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NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

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Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

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The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-30368. The polypeptides sequences are designated SEQ ID NO: 30369-60736. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

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The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO: 1-30368 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO: 1-30368. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-30368 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-30368. The sequence information can be a segment of any one of SEQ ID NO: 1-30368 that uniquely identifies or represents the sequence information of SEO ID NO: 1-30368.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-30368 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-30368 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO: 1-30368; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-30368. The polynucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-30368. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (e.g., SEQ ID NO: 30369-60736); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-30368; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention.

Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

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Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving abcrrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound that binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in the sequence listing). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

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It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

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The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 200 nucleotides. Preferably from about 20 nucleotides.

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NO: 1-30368.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

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The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO: 1-30368. The sequence information can be a segment of any one of SEQ ID NO: 1-30368 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO: 1-30368. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4²⁰ possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match $(1+4^{25})$ times the increased probability for mismatch at each nucleotide position (3×25) . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

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The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, proferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include an initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

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The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e g, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polypucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/jurnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, i.e., conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or

35 non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

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The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

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The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

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As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

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Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO: 1-30368; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO: 30369-60736; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 30369-60736. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-30368; (b) nucleotide sequences encoding any one of the amino acid sequences of SEQ ID NO: 1-30368; (b) nucleotide sequences cncoding any one of the amino acid sequences forth in the Sequence Listing; (c) a polynucleotide which is an allclic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 30369-60736.

Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic

domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

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The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-30368 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-30368 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-30368 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-30368, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that

are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

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The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-30368, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-30368 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-30368 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., Gene 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and Current Protocols in Molecular Biology, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-30368, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-30368 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-30368 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and

promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenical transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacl, lacZ, T3, T7, gpt. lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of 20 the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons 25 encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include E. coli, Bacillus subtilis, Salmonella typhimurium and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., Nat. Biotech. 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-30368, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEO ID

NO: 30369-60736 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-30368 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

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Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO: 1-30368), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylguanine, 2-methylguanine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylguanine, 5-methylguanine, 5-methylguanine, 5-methylguanine, 5-methylguanine, 5-methylguanine, 15-methoxymarinomethyl-2-thiouracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyl-2-thiouracil, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-3-d-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2.6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an -a nomeric nucleic acid molecule. An -a nomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO: 1-30368). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an mRNA of SEQ ID NO: 1-30368 (see, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742). Alternatively, polynucleotides of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991)

Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

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In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PMAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimcras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are the coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bloorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

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4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or

35 increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., Basic Methods in Molecular Biology (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals. mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

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The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA. allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO: 30369-60736 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-30368 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-30368 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 30369-60736 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 30369-60736 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 55%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%, 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 30369-60736.

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Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of theraneutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

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In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEO ID NO: 30369-60736.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequence can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to
35 retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether, or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form that will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His-tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY
AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al., ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

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The invention also provides chimeric or fusion proteins. As used herein, a "chimeric 35 protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

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For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction in vivo. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, e.g., cancer as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENETHERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The

homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

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The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art.

References disclosing such methods include without limitation "Molecular Cloning: A

Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning

Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokinc, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of soleen cells. Iymph node cells or

thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-y, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober.

Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

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Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypoptide of the invention

35 exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

4.10.6 TISSUE GROWTH ACTIVITY

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A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

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Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions that may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

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A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

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Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria. angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconiunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66. 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch, Toxocol, 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

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The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHID can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self-tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means

35 of up regulating immune responses, may also be useful in therapy. Upregulation of immune

responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the 30 following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA

78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

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Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in:
Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine
173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology
67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of
Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation
94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Finc et

al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polypueleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of

lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

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Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

35 4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermothcrapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a

35 portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or

modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D,

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Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2. Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors

and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

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The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the

35 novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

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Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see Science 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in in vivo tissue culture or animal models that are well known in the

art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

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The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for recentor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules. that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for recentor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The responses of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then

be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury. endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1. graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

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4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co. Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

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- traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries:
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system
 results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord
 15 infarction or ischemia:
 - (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
 - (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the 25 nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
- (vi) neurological lesions associated with systemic diseases including but not limited to
 diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or
 sarcoidosis:
 - (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or
 injured by a demyelinating disease including but not limited to multiple sclerosis, human

immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

increased survival time of neurons in culture;

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- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or in vivo, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eve

color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s), effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides).

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis are determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

30 4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

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4.11.1 EXAMPLE

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One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1 µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents

include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

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As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines. lymphokines or other

hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

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Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

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Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing. dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil. mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate

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to the barrier to be permeated are used in the formulation. Such penetrants are generally known

in the art.

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For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient. optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic. tale, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as tale or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or logenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliscr, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use

in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or cmulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may

be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B-lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

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The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 ug to about 100 mg (preferably about 0.1 ug to about 10 mg, more preferably about 0.1 ug to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally

capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

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The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the abovementioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hvaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

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Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (i.e., the concentration of

the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

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4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab}, F_{ab} and F_{(ab)2} fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses, and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 30369), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region on the surface of the protein of the invention that is located on the

surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

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For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypoptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corvnebacterium parvum, or similar immunostimulatory agents. Additional examples of

adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigenbinding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovinc and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the

culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

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Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, <u>Anal. Biochem.</u>, <u>107</u>:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium.

Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialvsis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells. Chinese hamster ovary (CHO) cells. or

myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

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The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab'), or other antigenbinding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" hercin. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 846 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from

the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fy molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

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5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{ab} fragment generated

by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

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Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodics with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol, 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcyR), such as FcyRI (CD64), FcyRII (CD32) and FcyRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

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Heteroconjugate antibodies are also within the scope of the present invention.

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond.

Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can

be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

5.13.8 Immunoconjugates

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The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include 212 Bi, 131 I, 131 In, 90 Y, and 186 Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

35 4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy dises, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-30368 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-30368 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

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As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited

to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

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In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

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Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents

include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide in vivo at the target site.

4.18 SCREENING ASSAYS

Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-30368, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
 - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

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The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design scquence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester,

ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - sce Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents that bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-30368. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO: 1-30368 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA

polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques. Percamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

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4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude et al. (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidatebond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

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The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidatebond is employed (Chu et al., (1983)) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidatebond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then strentavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C . After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodicster link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe

35 arrays may be employed. For example, addressable laser-activated photodeprotection may be

employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor et al. (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness et al. (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness et al. (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with evanuric chloride.

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One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease et al., (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected N-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook et al. (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer et al. (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of

these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed.

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genenic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the

subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

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5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Rapid Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

5.2 EXAMPLE 2

Novel Contigs

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The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-30368 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 115, gb pri 115, and UniGene version 103, and exons from public domain genomic sequences predicted by GenScan) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Further, the inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-30368) of the present invention are incorporated in the attached Sequence Listing. A subset the predicted polypeptide sequences contain an unknown amino acid, a stop codon, a possible nucleotide deletion or a possible nucleotide insertion. These sequences have been shown in their entirety with the special characters in Table 2. Table 2 also shows the corresponding start and stop nucleotide locations to each of SEQ ID NO: 1-30368. Table 2 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by

reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

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The nearest neighbor results for SEQ ID NO: 1-30368 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 121 and Geneseq release 200103 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-30368. The nearest neighbor results for SEQ ID NO: 1-30368 are incorporated in the attached Sequence Listing.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. The attached Sequence Listing provodes the results obtained by eMatrix analysis for each polypeptide as follows: the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. The attached Sequence Listing provides the results obtained by PFAM analysis for each peptide, namely: the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

Tables 1 and 2 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-30368.

Table 2 shows the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 2 also provides a correlation between the amino acid sequences set forth in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO: in USSN 09/540.217

Table 1

Tissue	RNA	Library	SEQ ID NOS:
origin	Source	Name	524 12 11051
adult brain	GIBCO	AB3001	39-41 192 197-200 315-316 540-542 576-580 608-622
			635 1004 1185-1187 1273-1279 1431 1474 1721-1722
			2036 2136-2137 2457 2471-2474 2513 2599-2603 2988-
			2989 3105-3106 3212 3276-3277 3306-3308 3352 3365
			3374-3376 3433 3448-3450 3555-3558 3693 3949-3953
			4067-4072 4160-4162 4558-4560 4581-4582 4612-4614
į.			4837-4840 5483-5484 5603-5606 5700 5802 5980-5984
	1		6135-6136 6403-6404 6452-6453 7209-7212 7447-7449
			7452-7460 7536-7541 7554-7555 7622-7623 7630-7636
			7660-7665 7701-7703 7771 7778-7783 7798-7801 7921-
			7923 7994 8010-8012 8025-8026 8145-8151 8227-8229
			8415 8497-8499 8936-8938 8986-8991 9002-9004 9013-
			9017 9337-9338 9366-9368 9375-9376 9391-9392 9395-
			9396 9431-9436 9443 9475-9476 9517-9518 9522-9525
	1		9586-9589 9603-9604 9851-9852 9854-9855 9874-9895
			9905-9908 9947-9952 9969-9980 9986-9992 10025-
			10026 10033-10037 10167-10172 10277 10480-10482
			10488-10489 10498-10503 10520-10522 10537-10538
1			10592-10594 10628-10630 11226-11227 11339-11344
			11406-11407 11431-11432 11731-11734 12150-12151
1	l		12239 12241-12244 12555-12559 12615-12618 12785-
1			12787 12978-12981 12984-12985 12997-12999 13567-
			13568 13592-13595 13606-13608 13873-13875 13999-
			14004 14360-14369 14650-14651 14684-14685 15013-
			15018 15096 15174-15181 15209-15210 15250-15251
			15257 15323-15324 15548-15552 15568-15572 15576-
1	1		15577 15588-15589 15699-15700 15881-15883 16438-
			16439 16473-16478 16496-16497 16609-16611 16686-
	1		16693 16700-16701 16727-16729 16836-16842 16934-
	ļ.		16937 16949-16953 17455-17456 17857-17861 17958-
			17963 18029-18030 18136-18138 18423-18425 18516-
			18518 18535-18537 18624-18626 18668-18672 18719-
			18722 18750-18756 18790-18793 18802-18804 18836-
1			18838 18899-18903 18919-18921 18943-18945 18947-
I			18950 18964-18969 18989-18990 19013-19017 19045-
			19048 19057-19065 19142-19147 19154-19155 19224
			19316-19317 19345-19349 19355-19360 19362 19370
			19385-19389 19415-19417 19422-19431 19442-19444
	İ		19503 19560-19562 19566 19604-19607 19693 19709-
			19710 19727-19732 19736-19742 19772 19804-19808
	1		19921-19929 19933-19938 19943-19946 19969-19981
	1		20015-20017 20029-20043 20087-20094 20099-20102
			20111-20112 20122-20127 20161-20164 20167-20171
1			20180-20181 20189-20194 20198-20199 20215-20218
			20281-20282 20289 20321-20324 20349-20354 20361
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Tissue	RNA	Library	SEQ ID NOS:
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			14685 14784 14789-14791 15182-15183 15257-15259
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Tissue	RNA	Library	SEQ ID NOS:
origin	Source	Name	
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			19808 19814-19822 19855-19856 19921-19929 19933-
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			19963 19965-19967 19972-19981 20015-20017 20029-
			20043 20048-20065 20074-20079 20087-20094 20099-
			20102 20106-20113 20120 20122-20127 20130-20132
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			20235-20240 20250-20253 20265-20270 20274-20278
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			20824-20849 20853-20854 20858-20863 20865 20881
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			20956 20963-20972 20977-20988 20991 20999-21004
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			21303 21326-21334 21340-21342 21351-21352 21377-
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	ļ.		22271-22289 22292-22299 22314-22318 22323-22328
			22333-22335 22343-22348 22358-22359 22365-22371
			22383-22388 22399-22408 22434-22435 22440-22448
			22495 22534-22539 22553-22558 22560 22571-22581
			22599-22602 22607-22609 22622-22628 22634-22643
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WO 01/075067			PCT/US01/08631
Tissue	RNA	Library	SEQ ID NOS:
origin	Source	Name	
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			27126 27147-27149 27209-27213 27229-27232 27269-
			27270 27275-27276 27414-27431 27439-27443 27468
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			1877 1879-1880 1884-1892 2015-2018 2370-2373 2516
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	}		5266 5337-5341 5530-5531 5846 6002-6004 6113 6226-
			6234 7618-7621 7745-7746 7794 7806-7808 7988 8041-
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			12432-12433 12760-12762 12872-12881 13609-13612
			13632-13633 14004 14048-14053 14058-14059 14105-
			14106 14170-14172 14207-14208 14546-14549 14604
		1	15290-15291 15491-15495 15588-15589 16434-16437
		į	16636-16637 16666-16667 16727-16733 17073 17455-
			17456 17958-17962 18527 18633-18637 18673-18677
			18796 18857-18880 18882-18888 18894-18896 18975
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	İ		19362 19370 19401-19402 19422-19431 19494-19496
			19749-19751 19764-19767 19953-19957 19962-19963
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			20441-20451 20472-20474 20548-20553 20631-20634
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WO 01/0			PCT/US01/08631
Tissue	RNA	Library Name	SEQ ID NOS:
origin	Source		27600-27601 27814-27815 27819-27820 28142-28145 28233 29367 30141-30142
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^{*}The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen),

4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

228

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nuclcotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	-	
1	30369	C	11	23	176	
2	30370	В	2	1	735	
3	30371	В	3	1	783	
4	30372	В	4	104	266	
5	30373	В	5	1	1113	
6	30374	C	6	3	164	
7	30375	В	7	112	279	
8	30376	В	8	198	405	
9	30377	В	9	1	687	
10	30378	c	10	346	598	
11	30379	В	11	1	960	
12	30380	В	12	44	350	
13	30381	В	13	264	465	
14	30382	В	14	483	1556	
15	30383	В	15	140	838	
16	30384	В	16	1	372	
17	30385	В	17	i	1404	
18	30386	В	18	25	2013	
19	30387	c	19	ī	381	
20	30388	c	20	605	755	
21	30389	В	21	1	912	
22	30390	c	22	124	315	
23	30391	c	23	44	310	
24	30392	В	24	1	330	
25	30393	В	25	î	411	
26	30394	В	26	147	257	
27	30395	В	27	i	597	
28	30396	В	28	201	862	
29	30397	c	29	249	515	
30	30398	В	30	41	816	
31	30399	С	31	26	142	
32	30400	В	32	259	2328	
33	30401	В	33	1	759	
34	30402	В	34	964	2121	
35	30403	C	35	298	449	
36	30404	c	36	115	396	
37	30405	С	37	148	318	
38	30406	С	38	383	483	
39	30407	В	39	1	1125	
40	30408	В	40	1	831	
41	30409	C	41	363	602	
42	30410	В	42	1	324	
43	30411	В	43	64	199	
44	30412	В	44	1	1007	
45	30413	C	45	380	583	
46	30414	В	46	1	432	
47	30415	ć	47	i	249	
48	30416	В	48	1	798	
49	30417	В	49	14	1070	
50	30418	c	50	1	225	
51	30419	В	51	1	2673	

229

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop cudon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				Sequence		
52	30420	В	52	ļi .	258	
53	30421	В	54	1	624	
54	30422	С	55	166	333	
55	30423	В	56	298	380	
56	30424	C	57	139	379	
57	30425	В	58	1	157	
58	30426	В	59	1	447	
59	30427	В	60	1	579	
60	30428	В	61	1	1059	
61	30429	В	62	1	816	
62	30430	В	63	1	558	
63	30431	В	64	1	540	
64	30432	В	65	1	555	
65	30433	В	66	1	648	
66	30434	В	67	1	798	
67	30435	В	68	1	1455	
68	30436	В	69	1	1278	
69	30437	В	70	88	3012	
70	30438	В	71	1	1092	7,32,7
71	30439	В	72	575	1033	
72	30440	В	73	644	926	
73	30441	В	74	1	1239	
74	30442	В	75	1	1074	
75	30443	В	76	81	467	
76	30444	С	77	44	286	
77	30445	В	78	1	297	
78	30446	В	79	1	978	
79	30447	В	80	72	715	
80	30448	В	81	1	1296	
81	30449	В	82	63	162	
82	30450	С	83	22	420	
83	30451	c	84	201	733	
84	30452	С	85	417	575	
85	30453	В	86	1	267	
86	30454	В	87	112	738	
87	30455	c	88	260	379	
88	30456	В	89	77	399	
89	30457	В	90	158	420	
90	30458	В	91	1	1437	
91	30459	c	92	22	321	
92	30460	В	93	1	843	
93	30461	В	94	142	2798	
94	30462	В	95	887	8434	
95	30463	В	96	1	1014	
96	30464	В	97	i i	1197	
97	30465	В	98	16	555	
98	30466	В	99	1	423	
99	30467	В	100	1	651	
100	30468	В	101	233	556	
101	30469	В	102	192	883	
102	30470	C	103	65	274	

SEO ID	Iceo in vo.	Tales	SEQ ID NO:	Nucleotide	Inveloptide location of last	Amino acid sequence (X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1.00	09/549,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
ŀ	1			sequence		·
		L_				
103	30471	С	104	328	546	
104	30472	В	105	80	3900	
105	30473	В	106	1	951	
106	30474	С	107	1	279	
107	30475	С	108	246	368	
108	30476	В	109	1	819	
109	30477	В	110	1	634	
110	30478	В	111	1	379	
111	30479	В	112	80	2747	
112	30480	С	113	139	414	
113	30481	С	114	1	330	
114	30482	В	115	53	618	
115	30483	В	116	1	426	
116	30484	С	117	135	296	
117	30485	С	118	239	432	
118	30486	С	119	381	776	
119	30487	В	120	1	381	
120	30488	c	121	42	175	
121	30489	c	122	1	399	
122	30490	В	123	i	792	
123	30491	В	124	1	894	
124	30492	В	125	1	3498	
125	30493	В	126	8	874	
126	30494	В	127	1	2160	
127	30495	В	128	i	1776	
128	30496	В	129	1	567	
129	30497	В	130	195	728	
130	30498	В	131	1	615	
131	30499	В	132	1	420	
132	30500	В	133	661	2711	
133	30501	B	134	1	621	
134	30502	c	136	i	465	
135	30503	c	137	113	502	
136	30504	c	139	78	269	
137	30505	c	140	98	472	
138	30506	В	141	403	533	
139	30507	c	142	64	315	
140	30508	В	143	1	591	
141	30509	c	144	528	1151	
142	30510	c	145	1	414	
143	30511	В	146		936	
144	30512	c	147	91	195	
144	30512	c	148	562	705	
145	30513	c	148	122	313	
147		В	150	566	1535	
	30515	C	150	75	248	
148		C	151	1	624	
149	30517				655	
150	30518	С	153	551		
151	30519	С	154	315	497 554	
152	30520	С	155	262		
153	30521	С	156	1	282	I

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	İ	1		sequence		
154	20522	 D	157	1	508	
154	30522	B C	158	243	545	
155	30523	-	159	8		
156	30524	B C	160	33	395 194	
157	30525			50		
158	30526	В	161	128	355	
159	30527	В	162	243	1230	
160	30528	B B	164	121	710 742	
161	30529			152		
162	30530	В	165		227	
163	30531	С	166	156	503	
164	30532	В	167	67	1280	
165	30533	В	168	1	444	
166	30534	В	169	161	206	
167	30535	В	170	189	1207	
168	30536	В	171	1	613	
169	30537	В	172	1	70	
170	30538	С	173	611	751	
171	30539	В	174	398	2472	
172	30540	В	175	87	646	
173	30541	В	176	1	1455	
174	30542	С	177	1	339	
175	30543	В	178	1	1458	
176	30544	В	179	278	766	
177	30545	В	181	85	749	
178	30546	В	182	50	498	
179	30547	С	183	1	522	
180	30548	В	184	90	482	
181	30549	В	185	86	442	
182	30550	С	187	129	308	
183	30551	С	188	1	414	
184	30552	В	190	1	378	
185	30553	С	192	252	308	
186	30554	В	193	1	576	
187	30555	С	194	1093	1311	
188	30556	В	195	45	324	
189	30557	В	196	1	249	
190	30558	С	197	309	443	
191	30559	С	198	615	866	
192	30560	В	199	86	1332	
193	30561	В	200	49	334	
194	30562	В	201	64	638	
195	30563	С	202	195	338	
196	30564	С	203	1	357	
197	30565	В	204	I	693	
198	30566	С	205	121	291	
199	30567	С	206	156	380	
200	30568	С	207	1211	1456	
201	30569	В	208	62	328	
202	30570	С	209	105	179	
203	30571	В	210	229	1483	
204	30572	В	211	1	749	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
205	30573	В	212	1	190	
206	30574	c -	213	121	367	
207	30575	В	214	121	456	
208	30576	В	215	1	2631	
209	30577	В	216	63	419	
210	30578	В	217	114	485	
211	30579	В	218	628	1447	
212	30580	C	219	252	377	
213	30581	В	220	1	847	
214	30582	В	221	68	343	
215	30583	В	222	138	911	
216	30584	В	223	44	882	
217	30585	В	224	1	429	
218	30586	В	225	87	312	
219	30587	C	226	44	343	
220	30588	c	227	41	286	· · · · · · · · · · · · · · · · · · ·
221	30589	C	228	1145	1372	
222	30590	В	229	1	720	
223	30591	c	230	i	430	
224	30592	c	231	58	297	
225	30593	В	232	613	683	
226	30594	В	233	613	683	
227	30595	c	234	238	455	
228	30596	В	235	319	615	
229	30597	c	236	255	494	
230	30598	В	237	106	600	
231	30599	В	238	i	654	
232	30600	В	239	1	654	
233	30601	В	240	243	356	
234	30602	В	241	1	932	
235	30603	c	242	36	215	
236	30604	В	243	1	288	
237	30605	C	244	25	186	·
238	30606	В	245	1	574	
239	30607	В	246	i	1257	
240	30608	В	247	162	263	
241	30609	C	248	79	207	
242	30610	В	249	194	276	
243	30611	В	250	1	1671	
244	30612	c	251	118	311	
245	30613	В	252	88	1485	
246	30614	В	253	339	443	
247	30615	В	254	667	1165	
248	30616	В	255	1	981	
249	30617	В	256	450	3131	
250	30617	В	257	900	1199	
251	30619	C	258	5	271	
252	30620	В	259	65	689	
253	30620	C	260	1	321	
254	30622	В	261	1	137	
255	30622	В	262	34	282	
233	120023	a	202	24	202	

SEQ ID	IEFO ID NO.	Mat	SEQ ID NO:	Nucleotide	Nucleotide teention of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.0.	sequence	liou.	09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
		1		sequence		
		L_				
256	30624	В	263	46	856	
257	30625	С	264	157	468	
258	30626	В	265	148	403	
259	30627	С	266	248	481	
260	30628	В	267	171	393	
261	30629	В	268	1	1078	
262	30630	В	269	1	550	
263	30631	В	270	I	1455	
264	30632	В	271	171	602	
265	30633	В	272	ī	1056	
266	30634	В	273	1	1101	
267	30635	В	274	1	2335	
268	30636	В	275	303	419	
269	30637	В	276	1	615	
270	30638	В	277	1	543	
271	30639	В	278	1	1602	
272	30640	С	279 -	585	1001	
273	30641	C	280	260	379	
274	30642	В	281	1	1437	
275	30643	С	282	22	321	
276	30644	В	283	1	843	
277	30645	В	284	142	2796	
278	30646	В	285	458	7217	
279	30647	В	286	84	186	
280	30648	С	287	67	229	
281	30649	С	288	15	245	
282	30650	С	289	125	232	
283	30651	В	290	1	594	
284	30652	В	291	376	670	
285	30653	C	292	82	405	
286	30654	В	293	35	651	
287	30655	В	294	56	487	
288	30656	c	295	313	498	- ,
289	30657	Ċ	296	118	261	
290	30658	В	297	198	1868	
291	30659	В	298	1	1665	
292	30660	c	299	73	108	
293	30661	В	300	1	408	
294	30662	В	301	i	444	
295	30663	В	302	8	311	
296	30664	c	303	144	350	
297	30665	В	304	1	669	
298	30666	c	305	416	820	
299	30667	В	306	253	837	
300	30668	В	307	44	475	
301	30669	В	308	185	885	
302	30670	C	309	206	337	
303	30670	В	310	1	393	.,
304	30672	В	311	1	1259	
305	30672	В	312	24	434	
306	30674	В	313	44	2687	
200	20074	IP.	213	77	2007	

SEQ ID	Tero In vo.	TM	SEQ ID NO:	Nucleatide	Newtonide leastion of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop endon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	ol' peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		· ·
307	30675	В	314	1	154	
308	30676	В	315	288	770	
309	30677	В	316	85	683	
310	30677	В	317	1	873	
311	30678	В	318	1	1737	
312	30680	С	319	1	690	
313	30681	В	320	58	1487	
314	30682	В	321	1	816	
		В	322	25	772	
315	30683			42		
316	30684	В	323		271	
317	30685	С	324	16	159	
318	30686	С	325	74	280	
319	30687	С	326	221	545	
320	30688	В	327	192	364	
321	30689	С	328	390	638	
322	30690	В	329	151	4215	
323	30691	В	330	1	2076	
324	30692	В	331	1	465	
325	30693	В	332	40	1350	
326	30694	В	333	1	489	
327	30695	В	334	285	744	
328	30696	С	335	96	347	
329	30697	С	336	213	326	•
330	30698	В	337	776	4384	
331	30699	В	338	201	317	
332	30700	В	339	1	2713	
333	30701	В	340	1	894	
334	30702	В	341	1	3842	
335	30703	С	342	745	1131	
336	30704	В	343	82	411	
337	30705	В	344	126	2123	
338	30706	В	345	57	1641	
339	30707	С	346	211	654	
340	30708	В	347	44	266	
341	30709	В	348	1	927	
342	30710	С	349	20	124	
343	30711	С	350	9	455	
344	30712	С	351	188	304	
345	30713	С	352	1	333	
346	30714	C	353	140	298	
347	30715	В	354	73	2171	
348	30716	В	355	1	1374	
349	30717	В	356	150	398	
350	30718	В	357	1	585	
351	30719	В	358	1	1716	
352	30720	В	359	81	1912	
353	30721	В	360	249	770	
354	30722	В	361	474	2875	
355	30723	С	362	1	483	
356	30724	C	363	1	251	
357	30725	C	364	28	407	

SEQ ID	SEC ID NO.	Later	SEQ ID NO:	Nucleotide	Nucleatide Incution of last	Aminu acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleutide insertion)
				sequence		
358	30726	C	365	88	204	
359	30727	В	366	474	684	
360	30728	С	367	41	394	
361	30729	В	368	253	1044	
362	30730	В	369	468	1111	
363	30731	В	370	1	558	
364	30732	В	371	21	345	
365	30733	В	372	1	744	
366	30734	В	373	1	795	
367	30735	В	374	1	685	
368	30736	В	375	94	414	
369	30737	С	376	86	268	
370	30738	В	377	1	1003	
371	30739	В	378	41	1385	
372	30740	В	379	1	510	
373	30741	В	380	40	746	
374	30742	В	381	100	1991	
375	30743	В	382	1	267	
376	30744	С	383	168	278	
377	30745	С	384	173	208	
378	30746	В	385	141	4538	
379	30747	В	386	1	4086	
380	30748	С	387	398	474	
381	30749	В	388	1	762	
382	30750	В	389	1	1584	
383	30751	В	390	1	2703	
384	30752	В	391	1	489	
385	30753	В	392	527	780	
386	30754	В	393	1	4050	
387	30755	В	394	859	2958	
388	30756	В	395	639	2307	
389	30757	В	396	ı	642	
390	30758	В	397	1	3639	
391	30759	В	398	219	540	
392	30760	В	399	1	3225	
393	30761	В	400	1	7552	
394	30762	С	401	626	1201	
395	30763	С	402	627	827	
396	30764	С	403	1	243	
397	30765	В	404	335	538	
398	30766	В	405	41	409	
399	30767	В	406	160	540	
400	30768	В	407	1	597	
401	30769	В	408	1	1605	
402	30770	В	409	1	351	
403	30771	В	410	65	601	
404	30772	В	411	1	870	
405	30773	В	412	91	2867	
406	30774	В	413	33	410	
407	30775	В	414	298	343	
408	30776	В	415	70	310	
	1			<u> </u>		

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	nou	09/540,217	codun for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
409	30777	В	416	64	1929	
410	30778	В	417	1	298	
411	30779	В	418	37	2612	
412	30780	В	419	1	510	
413	30781	В	420	44	1111	
414	30782	В	421	26	175	
415	30783	C	422	7	57	
416	30784	С	423	27	230	
417	30785	С	424	7	144	
418	30786	В	425	1	1746	
419	30787	С	426	318	486	
420	30788	В	427	896	1115	
421	30789	С	428	106	309	
422	30790	С	429	52	402	
423	30791	В	430	1	309	
424	30792	В	431 .	167	492	
425	30793	С	432	144	296	
426	30794	В	433	1	786	
427	30795	В	434	336	1303	
428	30796	В	435	333	419	
429	30797	В	436	1	489	
430	30798	С	437	1	199	
431	30799	С	438	110	239	
432	30800	С	439	175	303	
433	30801	С	440	35	181	
434	30802	В	441	1	1896	
435	30803	С	442	1	331	
436	30804	С	443	71	344	
437	30805	С	444	25	135	
438	30806	С	445	406	595	
439	30807	С	446	148	228	
440	30808	С	447	80	106	
441	30809	С	448	7	375	
442	30810	С	449	300	437	
443	30811	С	450	1	357	
444	30812	В	451	1	729	
445	30813	В	452	58	1287	
446	30814	С	453	1	410	
447	30815	С	454	1	411	
448	30816	С	455	1	420	
449	30817	В	456	1	555	
450	30818	В	457	376	1035	
451	30819	В	458	678	807	
452	30820	В	459	88	1485	
453	30821	В	460	300	2082	
454	30822	В	461	1	819	
455	30823	В	462	780	998	
456	30824	В	463	1	1871	
457	30825	В	464	1	1703	
458	30826	В	465	1	594	
459	30827	С	466	120	245	

SEQ ID	ICEO ID NO.	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
460	30828	C	467	1	387	
461	30828	В	468	<u> </u>	1678	
462	30830	В	469	1	533	
463	30831	В	470	347	656	
464	30832	В	471	1	1098	
465	30832	В	472	224	1518	
466	30834	C	473	44	244	
467	30835	В	474	1	1251	
468	30836	В	475	l i -	428	
469	30837	В	476	<u> </u>	495	
470	30838	C	477	233	373	
471	30839	В	478	8	950	
471	30840	C	479	1	813	
472	30841	В	480	1	1071	
474	30842	C	481	224	418	
475	30842	В	482	39	851	
476	30844	В	483	1	2006	
477	30844	В	484	1	561	
478		В	485	167	227	
479	30846 30847	В	486	1	777	
		В	487	1	645	
480	30848	В	488	1	1749	
481	30849	C	488	26		
482	30850	C	490	243	847 392	
483	30851					
484	30852	С	491	303	407	
485	30853	С	492	23	300	
486	30854	В	493	131	336	
487	30855	C	494	64	156	
488	30856	В	495	180	712	
489	30857		496 497	24	1104	
490	30858	В			917	
491	30859	В	498	65	228	
492	30860	В	499	1	2172	
493	30861	В	500	1	1338	
494	30862	В	501	1	795	
495	30863	C	502	181	410	
496	30864	В	503	69	1322	
497	30865	В	504	531	1315	
498	30866	С	505	24	320	
499	30867	В	506	1	791	
500	30868	В	507	1	3256	
501	30869	С	508	361	549	
502	30870	В	509	729	3252	
503	30871	В	510	424	1710	
504	30872	С	511	247	750	
505	30873	В	512	11	124	
506	30874	В	514	116	1079	
507	30875	В	515	1	766	
508	30876	В	516	185	796	
509	30877	В	517	1	456	
510	30878	В	518	99	435	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide inscrtion)
		1		scquence		\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
	100000	<u> </u>	1.0	ļ	loor	
511	30879 30880	В	519 520	54	834 246	
513	30880	В	521	1		
514	30881	C	522	78	372 305	
_		C	523	329		
515	30883 30884	В	524	1	484 459	
517	30885	В	525	630	889	
518	30886	В	526	95	343	
519	30887	В	527	353	610	
520	30888	В	528	113	529	
521	30889	В	529	362	1400	
522	30890	В	530	1	441	
523	30891	C	531	1	327	
524	30892	В	532	1	909	
525	30893	В	534	669	1268	
526	30894	В	535	293	826	
527	30894	C	536	12	155	
528	30896	c	537	1488	1706	
529	30897	c	538	26	211	
530	30898	c	539	30	185	
531	30899	В	540	1	789	
532	30900	В	541	63	358	
533	30901	В	542	1	900	
534	30902	В	543	1	728	
535	30903	В	544	112	220	
536	30904	В	545	49	386	
537	30905	В	546	1	585	
538	30906	В	547	328	531	
539	30907	В	548	10	987	
540	30908	В	549	49	248	
541	30909	В	550	131	368	
542	30910	В	551	80	1098	
543	30911	В	552	1	1364	
544	30912	В	553	1	1294	
545	30913	В	554	i	1995	
546	30914	В	555	i	279	
547	30915	В	556	175	715	
548	30916	В	557	1	636	
549	30917	В	558	1331	1600	
550	30918	В	559	32	406	
551	30919	В	560	38	206	
552	30920	В	561	1	1266	
553	30921	c	562	359	501	
554	30922	В	563	315	465	
555	30923	В	564	94	1683	
556	30924	В	565	1	1570	
557	30925	В	566	139	1734	
558	30926	В	567	1	810	
559	30927	В	568	658	1548	
560	30928	В	569	9	395	
561	30929	В	570	í i	567	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
562	30930	В	571	1	567	
563	30931	В	572	1	789	
564	30932	В	573	49	3187	
565	30933	В	574	1	1824	
566	30934	В	575	49	1413	
567	30935	В	576	1	1572	
568	30936	С	577	372	468	
569	30937	C	578	58	225	
570	30938	В	579	79	299	
571	30939	В	580	1	645	
572	30940	c	581	582	749	
573	30941	В	582	170	463	557 100
574	30942	В	583	311	520	
575	30943	В	584	1	1074	
576	30944	В	585	39	140	
577	30945	В	586	60	1685	
578	30946	В	587	106	879	
579	30947	С	588	67	362	
580	30948	В	589	45	126	
581	30949	С	590	1	390	
582	30950	С	591	49	240	
583	30951	В	592	1	496	
584	30952	В	593	94	482	
585	30953	C	594	12	341	
586	30954	В	595	1	354	
587	30955	В	596	1	711	
588	30956	В	597	123	412	
589	30957	В	598	1	1107	
590	30958	В	599	1	800	
591	30959	С	600	82	408	
592	30960	В	601	1	3174	
593	30961	В	602	1	444	
594	30962	В	603	1	1671	
595	30963	В	604	1	603	
596	30964	В	605	339	443	
597	30965	С	606	237	380	
598	30966	В	607	1	771	
599	30967	В	608	1	1767	
600	30968	С	609	1	801	
601	30969	В	610	1	1062	
602	30970	В	611	450	3131	
603	30971	С	612	178	435	
604	30972	С	613	164	319	
605	30973	С	614	1	385	
606	30974	C	615	392	853	
607	30975	С	616	24	200	
608	30976	С	617	34	327	
609	30977	В	618	1	624	
610	30978	В	619	179	1222	
611	30979	В	620	1	916	
612	30980	В	621	151	339	

SEO ID	SEQ ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleoride
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1			Į	sequence		
		<u> </u>				
613	30981	В	622	135	218	
614	30982	В	623	126	300	
615	30983	C	624	258	467	
616	30984	В	625	58	1038	
617	30985	В	626	246	4677	
618	30986	В	627	1	583	
619	30987	С	628	65	283	
620	30988	В	629	162	909	
621	30989	В	630	1	1062	
622	30990	В	631	1	909	
623	30991	С	632	160	297	
624	30992	В	633	352	1143	
625	30993	C	634	301	459	
626	30994	В	635	1	906	
627	30995	В	636	1	654	
628	30996	В	637	1	528	
629	30997	В	638	1	1102	
630	30998	С	639	81	299	
631	30999	В	640	1	345	
632	31000	В	641	39	360	
633	31001	В	642	22	293	
634	31002	С	643	1	504	
635	31003	В	644	107	3786	
636	31004	В	645	1	576	
637	31005	В	646	66	152	
638	31006	В	647	226	522	
639	31007	В	648	1	49	
640	31008	С	649	50	172	
641	31009	С	650	1	516	
642	31010	В	651	ĵi .	615	
643	31011	В	652	1	495	
644	31012	В	653	1	663	
645	31013	В	654	1	1812	
646	31014	В	655	1	1401	
647	31015	В	656	102	1151	
648	31016	В	657	1	385	
649	31017	В	658	232	987	
650	31018	В	659	1	1221	
651	31019	В	660	296	496	
652	31020	В	661	57	285	
653	31021	С	662	203	271	
654	31022	В	663	1	711	
655	31023	C	664	351	542	
656	31024	c	665	420	695	
657	31025	В	666	1	1860	
658	31026	В	667	71	2167	
659	31027	В	668	6	344	
660	31028	В	669	217	693	
661	31029	c	670	1	417	
662	31030	В	671	1	990	
663	31031	В	672	109	1169	
				L		

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
664	31032	C	673	40	117	
665	31032	C	674	301	560	
666	31033	В	675	1301	396	
667		В	676	483	1033	
668	31035 31036	В	677	673	3407	
669	31036	В	678	4	672	
		C	679	39	116	
670 671	31038	В	680	1	459	
672	31039	В	681	19	370	
		В	682	112	704	
673	31041	C	683	387	578	
674	31042	-				
675	31043	В	684	175	254	
676	31044	В	685	Li	501	
677	31045	В	686	290	389	
678	31046	В	687	1	486	
679	31047	В	688	1	651	
680	31048	В	689	181	401	
681	31049	В	690	117	406	
682	31050	В	691	1	169	
683	31051	В	692	1	1539	
684	31052	В	693	1	475	
685	31053	В	694	1	1575	
686	31054	В	695	1	507	
687	31055	В	696	1	498	
688	31056	С	697	253	492	
689	31057	В	698	1	588	
690	31058	В	699	75	291	
691	31059	В	700	1	1355	
692	31060	В	701	112	259	
693	31061	С	702	492	833	
694	31062	В	703	297	483	
695	31063	В	704	45	471	
696	31064	С	705	175	318	
697	31065	В	706	1	1074	
698	31066	В	7 07	94	1180	
699	31067	В	708	1	3866	
700	31068	C	709	215	424	
701	31069	В	710	1	499	
702	31070	В	711	210	325	
703	31071	В	712	1	786	
704	31072	В	713	l	777	
705	31073	В	714	174	1804	
706	31074	В	715	17	368	
707	31075	В	716	769	1831	
708	31076	В	717	76	301	
709	31077	В	718	1	825	
710	31078	С	719	1	396	
711	31079	В	720	93	2449	
712	31080	В	721	408	687	
713	31081	В	722	97	662	
714	31082	В	723	169	610	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
	ł			sequence		
715	31083	В	724	ī	2511	
716	31084	С	725	104	410	
717	31085	С	726	75	527	
718	31086	С	727	7	263	
719	31087	В	728	40	1725	
720	31088	В	729	290	1671	
721	31089	В	730	46	465	
722	31090	С	731	378	644	
723	31091	В	732	48	2331	
724	31092	В	733	1	738	
725	31093	В	734	1	1051	
726	31094	В	735	1	840	
727	31095	Ĉ	736	291	551	
728	31096	В	737	1	1308	
729	31097	В	738	1	291	
730	31098	С	739	1	702	
731	31099	В	740	1	379	
732	31100	В	741	80	2747	
733	31101	В	742	1	1992	
734	31102	В	743	293	1296	
735	31103	С	744	769	1017	
736	31104	С	745	166	294	
737	31105	В	746	928	1483	
738	31106	В	747	247	375	
739	31107	С	748	47	582	
740	31108	В	749	47	388	
741	31109	В	750	53	458	
742	31110	С	751	32	277	
743	31111	В	752	1	1641	
744	31112	С	753	1	483	
745	31113	В	754	1	1518	
746	31114	В	755	1	321	
747	31115	С	756	604	779	
748	31116	В	757	695	967	
749	31117	В	758	1	768	
750	31118	В	759	101	531	
751	31119	В	760	1	1014	
752	31120	С	761	424	564	
753	31121	В	762	1	333	
754	31122	В	763	15	165	
755	31123	В	764	1	555	
756	31124	В	765	344	476	
757	31125	В	766	1	648	
758	31126	В	767	1	981	
759	31127	С	768	22	162	
760	31128	В	769	1	225	
761	31129	В	770	232	1671	
762	31130	В	771	166	504	
763	31131	В	772	473	1694	
764	31132	С	773	232	414	
765	31133	С	774	374	463	

fero In	lero in vo-	154.4	SEQ ID NO:	Nucleatide	Nucleotide logotion of last	Amino acid sequence (X=Unknown,
SEQ ID NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
NO.	sequence	liou	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	orquence			sequence		
766	31134	В	775	1	1128	
767	31135	В	776	337	1284	
768	31136	С	777	25	282	
769	31137	C	778	4	63	
770	31138	c	779	496	1041	
771	31139	c	780	234	365	
772	31140	В	781	1	669	
773	31141	В	782	228	305	
774	31142	В	783	102	755	
775	31143	В	784	1	465	
776	31144	B	785	45	336	
777	31145	C	786	220	366	
778	31146	В	787	332	456	
779	31147	В	788	169	450	
780	31147	В	789	1	1173	
781	31149	В	790	36	355	
		C	791	354	482	
782	31150				708	
783	31151	С	792	328		
784	31152	В	793	1	829	
785	31153	В	794	14	182	
786	31154	В	795	307	1412	
787	31155	С	796	3	332	
788	31156	В	797	57	704	
789	31157	В	798	1	2406	
790	31158	С	799	1	759	
791	31159	В	800	1	351	
792	31160	В	801	142	272	
793	31161	В	802	34	2951	
794	31162	В	803	92	994	
795	31163	В	804	115	1746	
796	31164	С	805	292	408	
797	31165	В	806	1	880	
798	31166	С	807	156	329	
799	31167	С	808	119	328	
800	31168	С	809	1	492	
801	31169	В	810	1	516	
802	31170	В	811	1	624	
803	31,171	В	812	24	1868	
804	31172	С	813	164	208	
805	31173	С	814	91	249	
806	31174	В	815	1	1059	
807	31175	C	816	80	106	
808	31176	С	817	283	408	
809	31177	С	818	1	357	
810	31178	С	819	1	909	
811	31179	В	820	26	71	
812	31180	В	821	1	714	
813	31181	В	822	1	678	
814	31182	В	823	1	675	
815	31183	В	824	24	1046	
816	31184	В	825	1	933	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540.217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		0 2/13/40,217	sequence	of peptine sequence	actetion, i-possible interestine insertion)
817	31185	В	826	1	363	
818	31186	В	827	112	1655	
819	31187	В	828	1	417	
820	31188	В	829	88	1485	
821	31189	С	830	1	411	
822	31190	В	831	114	277	
823	31191	С	832	671	1039	
824	31192	В	833	63	342	
825	31193	В	834	3530	4798	
826	31194	В	835	1	333	
827	31195	В	836	1	831	
828	31196	В	837	1	2514	
829	31197	В	838	98	250	
830	31198	В	839	1	5247	
831	31199	В	840	1	531	
832	31200	В	841	167	466	
833	31201	В	842	160	417	
834	31202	В	843	215	380	
835	31203	В	844	706	1262	
836	31204	В	845	41	368	
837	31205	С	846	252	578	
838	31206	С	847	18	380	
839	31207	С	848	14	349	
840	31208	В	849	1	1176	
841	31209	В	850	244	1174	
842	31210	С	851	27	146	
843	31211	В	852	217	1866 .	
844	31212	В	853	98	242	
845	31213	В	854	52	2112	
846	31214	В	855	98	242	
847	31215	С	856	237	518	
848	31216	С	857	1	528	
849	31217	С	858	213	365	
850	31218	В	859	86	478	
851	31219	В	860	1	903	
852	31220	В	861	191	539	
853	31221	C	862	283	480	
854	31222	В	863	248	738	
855	31223	В	864	7	1602	
856	31224	В	865	113	375	
857	31225	В	866	50	435	
858	31226	В	867	50	646	
859	31227	В	868	1	2292	
860	31228	В	869	1	2385	
861	31229	В	870	184	852	
862	31230	В	871	1	408	
863	31231	В	872	218	484	
864	31232	В	873	90	588	
865	31233	В	874	445	625	
866	31234	В	875	138	618	
867	31235	В	876	1	753	
007	10.000	1	1	1.	1	

SEQ ID	leco in vo	154.4	SEQ ID NO:	North-Add-	Nt - tide location of lost	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1 '			sequence	' '	
		_				
868	31236	В	877	1	489	
869	31237	В	878	113	366	
870	31238	С	879	271	489	
871	31239	В	880	918	3257	
872	31240	В	881	185	631	
873	31241	C	882	3	194	
874	31242	В	883	80	3219	
875	31243	В	884	213	1835	
876	31244	С	885	132	224	
877	31245	В	886	1	741	
878	31246	С	887	132	224	
879	31247	В	888	1	1281	
880	31248	В	889	125	1910	
881	31249	В	890	1	1449	
882	31250	В	891	284	696	
883	31251	В	892	139	390	
884	31252	В	893	1	1308	
885	31253	В	894	1	594	
886	31254	В	895	1	678	
887	31255	В	896	19	240	
888	31256	В	897	47	330	
889	31257	В	898	1	388	
890	31258	В	899	52	564	
891	31259	С	900	310	672	
892	31260	В	901	1	1338	
893	31261	c	902	77	214	
894	31262	С	903	213	467	
895	31263	c	904	202	426	
896	31264	В	905	68	567	
897	31265	С	906	32	205	
898	31266	c	907	513	701	
899	31267	В	908	1	1083	
900	31268	В	909	787	1633	
901	31269	С	910	40	288	
902	31270	В	911	178	330	
903	31271	В	912	129	520	
904	31272	В	913	2267	2626	
905	31273	c	914	34	87	
906	31274	В	915	23	610	
907	31275	В	916	1	1011	
908	31276	В	917	1	156	
909	31277	В	918	i	754	
910	31278	В	919	1	679	
911	31279	В	920	149	761	
912	31280	В	921	38	1175	
913	31281	c	922	542	724	
914	31282	В	923	31	283	
914	31283	В	923	21	341	
916	31284	В	925	199	361	
917	31285	В	926	293	427	
917	31285	В	927	56	145	
710	31200	lo_	747	150	1145	L

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
919	31287	В	928	21	341	
920	31288	В	929	199	361	
921	31289	В	930	293	427	
921	31289	В	931	305	465	
922	31290	B	932	280	457	
		C	932	45	562	
924	31292					
925	31293	В	934	130	618	
926	31294	В	935	418	1620	
927	31295	В	936	115	252	
928	31296	В	937	1	573	
929	31297	В	938	1	2661	
930	31298 .	В	939	1	1345	
931	31299	С	940	747	1220	
932	31300	С	941	249	429	
933	31301	В	942	1	363	
934	31302	С	943	390	589	
935	31303	В	944	437	1553	
936	31304	В	945	1	1521	
937	31305	С	946	84	347	
938	31306	В	949	80	315	
939	31307	В	950	1	537	
940	31308	c	951	181	330	
941	31309	c	952	55	123	
942	31310	c	953	52	195	
943	31311	c	954	55	123	_
944	31312	В	955	336	648	
945	31313	В	956	1	894	
946	31314	В	957	239	1008	
947	31315	В	958	126	308	
947	31316	В	959	1	747	
949		В	960	101	351	
	31317					
950	31318	В	961	179	1161	
951	31319	В	962	1	138	
952	31320	В	963	8	791	
953	31321	С	964	218	358	
954	31322	С	965	155	454	
955	31323	С	966	124	303	
956	31324	С	967	1	246	
957	31325	В	968	208	364	
958	31326	С	969	95	256	
959	31327	С	970	312	467	
960	31328	В	971	92	424	
961	31329	В	972	88	147	
962	31330	C	973	434	775	
963	31331	В	974	26	1781	
964	31332	С	975	363	692	
965	31333	В	976	201	563	
966	31334	В	977	348	687	
967	31335	C	978	529	660	
968	31336	c	979	418	738	
969	31337	c	980	25	177	
1202	101001	1~	1,00	1~~	1	1

SEQ ID	lero in vo.	Tates	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1.00	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
970	31338	В	981	308	388	
971	31339	С	982	230	580	
972	31340	В	983	101	342	
973	31341	В	984	1	2341	
974	31342	С	985	1	642	
975	31343	В	986	1	1173	
976	31344	В	987	39	6743	
977	31345	В	988	1	516	
978	31346	В	989	1	756	
979	31347	В	990	1	912	
980	31348	В	991	310	441	
981	31349	C	992	58	300	
982	31350	В	993	80	1344	
983	31351	С	994	325	414	
984	31352	В	995	80	1582	
985	31353	С	996	143	499	
986	31354	В	997	173	375	
987	31355	С	998	126	268	
988	31356	В	999	1	762	
989	31357	В	1000	1	642	
990	31358	В	1001	1	1980	
991	31359	В	1002	67	456	
992	31360	В	1003	48	335	
993	31361	В	1004	l	1251	
994	31362	В	1005	1	642	
995	31363	В	1006	1	570	
996	31364	С	1007	1	687	
997	31365	В	1008	1	5450	
998	31366	В	1009	586	852	
999	31367	В	1010	299	530	
1000	31368	В	1011	1	1659	
1001	31369	В	1012	2	550	
1002	31370	С	1013	2	97	
1003	31371	В	1014	1114	1476	
1004	31372	В	1015	22	822	
1005	31373	С	1016	646	903	
1006	31374	C	1017	1	351	
1007	31375	В	1018	226	1284	
1008	31376	В	1019	138	997	
1009	31377	В	1020	341	527	
1010	31378	В	1021	157	1415	
1011	31379	В	1022	55	211	
1012	31380	В	1023	55	211	
1013	31381	С	1024	18	197	
1014	31382	В	1025	1	876	
1015	31383	В	1026	276	487	
1016	31384	В	1027	1	294	
1017	31385	В	1028	273	377	
1018	31386	В	1029	1	936	
1019	31387	В	1030	1	1158	
1020	31388	С	1031	104	283	

SEQ ID	ICEO ID NO.	Dist	SEQ ID NO:	Nucleotide	In unlantide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codou, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	l '	1		sequence		
	101000	<u> </u>	11022		Igo	
1021	31389	В	1032	1	720	
1022	31390	В	1033	1	219	
1023	31391	В	1034	1	170	
1024	31392	В	1035	300	831	
1025	31393	С	1036	1	456	
1026	31394	В	1037	1	1149	
1027	31395	В	1038	1	627	
1028	31396	В	1039	161	375	
1029	31397	В	1040	1	360	
1030	31398	В	1041	1	549	
1031	31399	В	1042	1	384	
1032	31400	В	1046	1	675	
1033	31401	С	1047	379	675	
1034	31402	В	1048	166	388	
1035	31403	В	1049	26	66	
1036	31404	В	1050	1	897	
1037	31405	В	1051	30	1359	
1038	31406	В	1052	1	990	
1039	31407	В	1053	52	1507	
1040	31408	С	1054	66	290	
1041	31409	В	1055	158	2072	
1042	31410	В	1056	1	654	
1043	31411	В	1057	51	1143	
1044	31412	С	1058	66	290	
1045	31413	В	1059	547	1510	
1046	31414	В	1060	1	1499	
1047	31415	В	1061	1	3347	
1048	31416	С	1062	116	235	
1049	31417	В	1063	1	1185	
1050	31418	С	1064	221	823	
1051	31419	В	1065	235	359	
1052	31420	С	1066	1	360	
1053	31421	В	1067	49	386	
1054	31422	С	1068	63	383	
1055	31423	В	1069	60	213	
1056	31424	В	1070	1	919	
1057	31425	В	1071	294	557	
1058	31426	В	1072	1	486	
1059	31427	В	1073	I	450	
1060	31428	С	1074	28	207	
1061	31429	В	1075	1	585	
1062	31430	В	1076	60	213	
1063	31431	В	1077	18	457	
1064	31432	В	1078	112	177	
1065	31433	C	1079	1	375	
1066	31434	В	1080	39	91	
1067	31435	В	1081	91	237	
1068	31436	В	1082	255	376	
1069	31437	В	1083	18	431	
1070	31438	В	1084	98	552	
1071	31439	В	1085	1679	1964	
		1		1 - 1		·

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
1072	31440	В	1086	132	1200	
1073	31441	В	1087	95	418	
1074	31442	В	1088	26	56	
1075	31443	В	1089	1	873	
1076	31444	c	1090	107	196	-
1077	31445	В	1091	157	777	
1078	31446	В	1092	1	1273	**
1079	31447	В	1093	1	202	
1080	31448	B	1094	1	382	
1081	31449	c	1095	189	449	
1082	31450	c	1096	325	429	
1083	31451	c	1097	3	80	
1084	31452	B	1098	50	691	
1085	31453	В	1099	1	474	
1086	31454	В	1100	3	335	
1087	31455	В	1101	137	617	
1088	31456	c	1102	69	134	
1089	31457	В	1103	369	886	
1090	31458	В	1104	1	1332	
1091	31459	В	1105	106	584	
1091	31460	c	1106	97	420	
1092	31461	c	1107	142	381	
1094	31462	В	1108	214	2544	
1095	31463	В	1109	238	1323	
1095	31464	В	1110	1	3000	
1097	31465	В	1111	203	313	
1098	31466	В	1112	288	375	
1099	31467	В	1113	1	480	
1100	31468	c	1114	286	351	
1101	31469	В	1115	59	376	
1102	31470	c	1116	287	504	
1102	31471	В	1117	878	2032	
1104	31472	В	1118	52	648	
1105	31473	В	1119	1	207	
1106	31474	c	1120	í —	492	
1107	31475	В	1121	46	830	*****
1108	31476	В	1122	1	525	
1109	31477	В	1123	i	930	
1110	31478	c	1124	157	606	
1111	31479	c	1125	70	405	
1112	31480	c	1126	247	411	
1113	31481	c	1127	339	590	
1114	31482	В	1128	1	1881	
1115	31483	c	1129	258	452	
1116	31484	В	1130	241	733	
1117	31485	C	1131	294	530	
1118	31486	В	1132	1	439	
1119	31487	В	1132	16	612	
1120	31488	C	1133	234	377	
1121	31489	В	1134	134	763	
1122	31490	C	1136	1	228	
1122	151450	1	11130	11	220	

fore to	Torre to tre	124	leco in vo	No. of contrast	Inc. A. of A. Landon of Land	I - to the residence (V - t) - to -
SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	location of first	codon for last amino acid	Amino acid sequence (X=1/nknown, *=Stop codon, /=possible nucleotide
NO.	sequence	liou	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
				·		
1123	31491	В	1137	63	443	
1124	31492	С	1138	30	269	
1125	31493	В	1139	44	151	
1126	31494	В	1140	69	199	
1127	31495	В	1141	347	2830	
1128	31496	В	1142	1	576	
1129	31497	c	1143	49	129	
1130	31498	В	1144	1	1107	
1131	31499	В	1145	17	153	
1132	31500	В	1146	277	694	
1133	31501	В	1147	1	735	
1134	31502	В	1148	1	1110	
1135	31503	В	1149	55	552	
1136	31504	c	1150	463	591	
1137	31505	В	1151	136	266	
1138	31506	В	1152	1	795	
1139	31507	В	1153	128	880	
1140	31508	c	1154	178	366	
1141	31509	В	1155	1	654	
1142	31510	В	1156	1	3294	
1143	31511	В	1157	16	854	
1144	31512	В	1158	1093	1185	
1144	31512	В	1159	1	930	
1146	31514	В	1160	1	3969	
1147	31515	В	1161	1	4173	
1148	31516	В	1162	1	2187	
1149	31517	В	1163	47	993	
1150	31518	В	1164	1	1241	
1151	31519	В	1165	46	2170	
1152	31520	В	1166	1	1781	
1153	31521	В	1167	179	583	
1154	31521	C	1168	167	442	
1155	31523	В	1169	44	1848	
1156	31524	c	1170	1	417	
1157	31525	В	1171	i -	198	
1158	31526	В	1172	231	452	
1158	31526	В	1172	219	326	
1160	31527	В	1173	212	302	
1161	31528	В	1174	748	1084	
				1/48	540	
1162	31530	В	1176			
1163	31531	С	1177	21	143	
1164	31532	В	1178	76	1300	
1165	31533	В	1179	1	1324	
1166	31534	В	1180	1	1065	
1167	31535	В	1181	1	1263	
1168	31536	В	1182	1	1809	
1169	31537	В	1183	10	406	
1170	31538	В	1184	65	287	
1171	31539	В	1185	25	337	
1172	31540	В	1186	59	698	
1173	31541	C	1187	329	527	

SEO ID	lero in vo	133.4	SEQ ID NO:	Nucleotide	Northeside lossesion of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
10.	sequence	1100	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	,			sequence		
1174	31542	В	1188	1	1068	
1175	31543	В	1189	72	330	
1176	31544	В	1190	14	239	
1177	31545	В	1191	1	919	
1178	31546	В	1192	462	786	
1179	31547	В	1193	1	3468	
1180	31548	В	1194	16	457	
1181	31549	В	1195	1	697	
1182	31550	C	1196	1	145	
1183	31551	В	1197	91	450	
1184	31552	В	1198	1	1050	
1185	31553	В	1199	101	428	
1186	31554	В	1200	41	205	
1187	31555	В	1201	358	1082	
1188	31556	В	1202	1	183	-
1189	31557	В	1203	i	1053	
1190	31558	В	1204	73	336	
1191	31559	В	1205	553	1587	
1192	31560	C	1206	118	366	
1193	31561	В	1207	1	423	
1194	31562	В	1208	120	338	
1194	31563	В	1209	1	1665	
1196	31564	В	1210	1	639	
1197	31565	В	1211	1	660	
1197	31566	В	1212	11	434	
1199	31567	В	1213	1	567	
1200	31568	В	1214	1	801	
1200	31569	С	1215	56	177	
1201	31570	В	1216	439	678	
1202	31571	В	1217	20	201	
1204	31572	В	1218	74	267 325	
1205	31573	В	1219			
1206	31574	В	1220	37	340	
1207	31575	В	1221	1	588	
1208	31576	В	1222	136	294	
1209	31577	В	1223	238	392	
1210	31578	В	1224	109	1394	
1211	31579	С	1225	300	653	
1212	31580	В	1226	32	3327	
1213	31581	В	1227	497	1306	
1214	31582	С	1228	1	333	
1215	31583	С	1229	1	249	
1216	31584	С	1230	1	249	
1217	31585	В	1231	147	297	
1218	31586	В	1232	1	714	
1219	31587	В	1233	1	1587	·
1220	31588	С	1234	103	243	
1221	31589	С	1235	133	509	
1222	31590	В	1236	1	1594	
1223	31591	В	1237	1	628	
1224	31592	В	1238	1	948	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
1225	31593	В	1239	382	1020	
1226	31594	В	1240	163	5459	
1227	31595	В	1241	ı	1386	
1228	31596	В	1242	44	344	
1229	31597	В	1243	6	398	
1230	31598	В	1244	77	468	
1231	31599	В	1245	520	2001	
1232	31600	В	1246	1	645	
1233	31601	В	1247	91	690	
1234	31602	В	1248	70	382	
1235	31603	В	1249	183	427	
1236	31604	В	1250	159	621	
1237	31605	В	1251	34	259	
1238	31606	В	1252	155	496	
1239	31607	В	1253	1	1416	
1240	31608	С	1254	18	355	
1241	31609	С	1255	665	826	
1242	31610	В	1256	1	559	
1243	31611	В	1257	343	1329	
1244	31612	В	1258	1	265	
1245	31613	В	1259	1	5081	
1246	31614	В	1260	373	1395	
1247	31615	В	1261	83	373 .	
1248	31616	В	1262	298	1252	
1249	31617	С	1263	142	327	
1250	31618	В	1264	1	237	
1251	31619	С	1265	1	330	
1252	31620	С	1266	20	358	
1253	31621	С	1267	347	493	
1254	31622	В	1268	220	1314	-
1255	31623	В	1269	1	1244	
1256	31624	В	1270	35	368	
1257	31625	В	1271	145	444	
1258	31626	В	1272	1	657	
1259	31627	В	1273	84	273	
1260	31628	С	1274	47	148	
1261	31629	В	1275	1	528	
1262	31630	В	1276	34	1370	
1263	31631	С	1277	81	299	
1264	31632	С	1278	22	201	
1265	31633	В	1279	1	672	
1266	31634	В	1280	1	753	
1267	31635	С	1281	14	79	
1268	31636	С	1282	61	227	
1269	31637	В	1283	95	1124	
1270	31638	В	1284	1	891	
1271	31639	В	1285	1	1323	
1272	31640	В	1286	11	127	
1273	31641	В	1287 ·	281	437	
1274	31642	С	1288	62	136	
1275	31643	В	1289	251	874	

SEQ ID	lero in No.	later	SEQ ID NO:	Nuclearite	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon,/=possible nuclcotide
1	sequence	1.00	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1		l		sequence	' ' '	
1276	31644	С	1290	16	231	
1277	31645	С	1291	299	412	
1278	31646	В	1292	310	968	
1279	31647	В	1293	237	1802	
1280	31648	В	1294	337	1143	
1281	31649	С	1295	75	176	
1282	31650	С	1296	193	414	
1283	31651	С	1297	98	679	
1284	31652	В	1298	186	260	
1285	31653	В	1299	1	732	
1286	31654	В	1300	123	268	
1287	31655	С	1301	1	420	
1288	31656	C	1302	86	223	
1289	31657	В	1303	1	594	
1290	31658	В	1304	1	4464	
1291	31659	c	1305	i	531	
1292	31660	В	1307	i	780	
1293	31661	c	1308	i	249	
1294	31662	В	1309	1	139	
1295	31663	В	1310	i	156	
1296	31664	В	1311	38	403	
1297	31665	В	1312	128	1089	
1298	31666	c	1313	262	429	
1299	31667	c	1314	209	592	
1300	31668	В	1315	1	684	
1301	31669	С	1316	i	339	
1302	31670	c	1317	71	310	
1302	31671	В	1318	1	476	
1304	31672	В	1319	133	198	
1305	31673	В	1320	1	227	
1306	31674	c	1321	612	977	
1307	31675	c	1322	65	523	
1307	31676	c	1323	35	121	
1309	31677	В	1324	8	430	
1310	31678	C	1325	1	438	
1311	31679	В	1326	1935	3296	
1311		В	1332	254	462	
1312	31680	В	1333	1006	1540	-
1314		В	1335	127	1799	
	31682	В		221	402	
1315	31683		1336	1		
1316	31684	C	1337	•	567	
1317	31685	С	1338	193	342	
1318	31686	В	1339	652	775	
1319	31687	В	1340	1	552	
1320	31688	В	1341	83	318	
1321	31689	В	1342	166	352	
1322	31690	C	1343	1	228	
1323	31691	В	1344	25	244	
1324	31692	С	1345	58	285	
1325	31693	В	1346	34	822	
1326	31694	В	1347	1	1563	

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
1327	31695	В	1348	229	1185	
1328	31696	В	1349	59	819	
1329	31697	В	1350	i	5955	
1330	31698	В	1351	i	654	
1331	31699	В	1352	i -	1299	
1332	31700	В	1353	943	1872	
1333	31701	В	1354	1	942	
1334	31702	В	1355	444	560	
1335	31703	В	1356	1	1605	
1336	31704	В	1357	1	831	
1337	31705	C	1358	48	383	
1338	31706	c	1359	1	318	
1339	31707	В	1360	186	470	
1340	31708	c	1361	ı	321	
1341	31709	В	1362	1	720	
1342	31710	В	1363	1	939	
1343	31711	B	1364	1	576	
1344	31712	В	1365	1	114	
1345	31713	В	1366	129	588	
1346	31714	В	1367	24	724	
1347	31715	В	1368	1	1840	
1348	31716	В	1369	14	350	
1349	31717	В	1370	1	3187	
1350	31718	С	1371	1	261	
1351	31719	В	1372	117	890	
1352	31720	В	1373	1	438	
1353	31721	В	1374	1	217	
1354	31722	В	1375	1	160	
1355	31723	С	1376	6	191	
1356	31724	В	1377	1	759	
1357	31725	В	1378	10	251	
1358	31726	В	1379	1	719	
1359	31727	С	1380	425	886	
1360	31728	С	1381	1	216	
1361	31729	С	1382	38	229	
1362	31730	В	1383	38	672	
1363	31731	В	1384	1	1845	
1364	31732	В	1385	1	2590	
1365	31733	B_	1386	32	108	
1366	31734	c_	1387	215	460	
1367	31735	В	1388]	1008	
1368	31736	В	1389	1	368	
1369	31737	В	1390	44	2402	
1370	31738	В	1391	80	1617	
1371	31739	С	1392	199	531	
1372	31740	В	1393	1	465	
1373	31741	C_	1394	415	612	
1374	31742	В	1395	16	147	
1375	31743	В	1396	1	1314	
1376	31744	В	1397	1	465	
1377	31745	В	1398	1	1569	

SEQ ID	ISEO ID NO.	Mat	SEQ ID NO:	Nucleotide	Nucleatide Incation of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
			<u></u>			
1378	31746	В	1399	1	490	
1379	31747	В	1400	405	573	
1380	31748	В	1401	1	2106	
1381	31749	В	1402	1	1593	
1382	31750	В	1403	1	666	
1383	31751	В	1404	1	652	
1384	31752	В	1405	352	1239	
1385	31753	В	1406	1	3184	
1386	31754	В	1407	467	1433	
1387	31755	В	1408	95	428	
1388	31756	С	1409	164	208	
1389	31757	С	1410	118	511	
1390	31758	С	1411	339	431	
1391	31759	В	1412	1	396	
1392	31760	В	1413	1	663	
1393	31761	В	1414	1	864	
1394	31762	С	1415	1	471	
1395	31763	В	1416	1	642	
1396	31764	В	1417	594	1764	
1397	31765	В	1418	1	771	
1398	31766	В	1419	1	5131	
1399	31767	В	1420	60	617	
1400	31768	В	1421	587	1202	
1401	31769	С	1422	336	638	
1402	31770	С	1423	30	200	
1403	31771	В	1424	1	1363	
1404	31772	В	1425	1	1113	
1405	31773	В	1426	1	1101	
1406	31774	В	1427	575	805	
1407	31775	C	1428	1	149	
1408	31776	c	1429	1	294	
1409	31777	c	1430	228	469	
1410	31778	В	1431	182	518	
1411	31779	В	1432	239	448	
1412	31780	В	1433	1	434	
1413	31781	C	1434	24	290	
1414	31782	c	1435	334	459	
1415	31783	В	1436	69	320	
1416	31784	В	1437	1	426	
1417	31785	В	1438	605	1423	
1418	31786	c	1439	9	113	
1419	31787	В	1440	1	58	
1420	31788	В	1441	1	210	
1421	31789	В	1442	1	2985	
1422	31790	C	1443	152	292	
1423	31791	В	1444	57	849	
1423	31792	C	1445	41	142	<u> </u>
1424	31793	c	1446	38	341	
1425	31794	c	1446	220	450	
1426	31795	c	1448	154	469	
1427	31796	В	1448	139	1023	
1420	151790	Ιο	1997	137	1023	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon fur last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
1429	31797	В	1450	55	2370	
1430	31798	В	1451	1	1707	
1431	31799	В	1452	566	2356	
1432	31800	В	1453	72	255	
1433	31801	В	1454	51	182	
1434	31802	В	1455	466	600	
1435	31803	В	1456	481	1209	
1436	31804	В	1457	1	1638	
1437	31805	В	1458	8	874	
1438	31806	В	1459	1	552	
1439	31807	В	1460	1	2566	
1440	31808	В	1461	85	270	
1441	31809	В	1462	159	392	
1442	31810	В	1463	88	459	
1443	31811	В	1464	131	406	
1444	31812	В	1465	69	194	
1445	31813	В	1466	59	3134	
1446	31814	В	1467	1	3097	
1447	31815	В	1468	328	519	
1448	31816	С	1469	40	436	
1449	31817	В	1470	1	981	
1450	31818	В	1471	30	285	
1451	31819	В	1475	93	932	
1452	31820	В	1476	1	369	
1453	31821	С	1477	102	227	
1454	31822	В	1478	613	679	
1455	31823	В	1479	51	587	
1456	31824	С	1480	3	188	
1457	31825	В	1481	1	1434	
1458	31826	С	1482	27	173	
1459	31827	С	1483	294	503	
1460	31828	С	1484	506	718	
1461	31829	С	1485	97	504	
1462	31830	C	1486	27	185	
1463	31831	В	1487	50	3247	
1464	31832	В	1488	1	1032	
1465	31833	В	1489	8	95	
1466	31834	В	1490	17	303	
1467	31835	В	1491	34	81	
1468	31836	В	1492	1	1110	
1469	31837	В	1493	1	928	
1470	31838	C	1494	498	704	
1471	31839	В	1495	4	747	
1472	31840	В	1496	1	933	
1473	31841	В	1497	137	687	
1474	31842	В	1498	1524	1676	
1475	31843	В	1499	1	156	
1476	31844	В	1500	1	1126	
1477	31845	В	1501	122	765	
1478	31846	В	1503	95	304	
1479	31847	В	1504	1	156	
1472	12/04/	10	1.504		150	

SEQ ID	ISEO ID NO.	Mat	SEQ ID NO:	Nucleotido	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	cudon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
1480	31848	C	1505	12	173	
1481	31849	В	1506	10	252	
1481		В	1507	25	301	
1483	31850	В	1508	34	267	
1484		В	1509	10	366	
1485	31852	В	1510	536	2776	
1486	31854	В	1511	1	276	
1487	31855	В	1512	i	420	
1488	31856	В	1513	235	363	
1489	31857	В	1514	664	741	
1490	31858	C	1515	312	452	
1491	31859	В	1516	1	504	
1492	31860	В	1517	52	346	
1493	31861	В	1518	458	1283	
1493	31862	В	1519	324	473	
1495	31863	В	1520	137	286	
1496	31864	В	1521	1	2682	
1497	31865	В	1522	352	1132	
1498	31866	В	1523	245	397	
1499	31867	c	1524	371	661	
1500	31868	В	1525	69	325	
1501	31869	B	1526	38	997	
1502	31870	В	1527	1	1753	
1503	31871	В	1528	215	2588	
1504	31872	c	1529	38	124	
1505	31873	c	1530	33	317	
1506	31874	c	1531	224	379	
1507	31875	В	1532	1	480	
1508	31876	c	1533	145	256	
1509	31877	Ċ	1534	64	198	
1510	31878	В	1535	1	394	
1511	31879	C	1536	1	696	
1512	31880	В	1537	67	246	
1513	31881	c	1538	95	253	
1514	31882	В	1539	145	476	
1515	31883	c	1540	1	361	
1516	31884	c	1541	1	276	
1517	31885	В	1542	1	658	
1518	31886	В	1543	1	623	
1519	31887	С	1544	187	465	
1520	31888	С	1545	1	207	
1521	31889	С	1546	24	512	
1522	31890	C	1547	20	121	
1523	31891	В	1548	1	785	
1524	31892	В	1549	1	498	
1525	31893	С	1550	17	118	
1526	31894	С	1551	1	291	
1527	31895	В	1552	1	504	
1528	31896	В	1553	62	413	
1529	31897	В	1554	1	282	
1530	31898	С	1555	236	408	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1531	31899	С	1556	220	398	
1532	31900	c	1557	1	732	
1533	31901	c	1558	i -	372	
1534	31902	В	1559	1	1086	
1535	31903	c	1560	286	642	
1536	31904	В	1561	8 .	339	
1537	31905	В	1562	16	88	
1538	31906	c	1563	227	405	
1539	31907	В	1564	253	693	
1540	31908	C	1565	1	129	
1541	31909	В	1566	li	390	
1542	31910	В	1567	1	1377	
1543	31911	c	1568	16	264	
1544	31912	c	1569	51	269	
1545	31912	c	1570	39	266	
1546	31913	В	1571	200	260	
1547	31914	В	1572	220	372	
1548	31916	В	1573	1	377	
1548	31917	C	1574	280	441	
1550	31917	C	1575	50	131	
1551	31918	c	1576	47	265	
				10	291	
1552	31920	С	1577		522	
1553	31921	В	1579	1	1166	
1554	31922	В	1580	756 382	1228	
1555	31923				229	
1556	31924	В	1581	63		
1557	31925	В	1582	1	452	
1558	31926	С	1583	299	556	
1559	31927	В	1584	1	870	
1560	31928	В	1585	1	708	
1561	31929	С	1586	1	420	
1562	31930	В	1587	1	1011	
1563	31931	C	1588	84	176	
1564	31932	С	1589	52	201	
1565	31933	С	1590	55	154	
1566	31934	С	1591	1	390	
1567	31935	С	1592	15	317	
1568	31936	В	1593	1	501	
1569	31937	В	1594	306	398	
1570	31938	В	1595	204	402	
1571	31939	С	1596	30	155	
1572	31940	В	1597	1	2274	
1573	31941	В	1598	1	486	
1574	31942	С	1599	148	504	
1575	31943	С	1600	82	282	
1576	31944	С	1601	82	282	
1577	31945	В	1602	66	395	
1578	31946	В	1603	114	237	
1579	31947	В	1604	1	1326	
1580	31948	В	1605	1	1900	
1581	31949	В	1606	1	1548	

SEQ ID	SEO ID NO.	Mer	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence (X=Unknown,
SEQ ID NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
l	1 '	ĺ	l .	sequence		
				L		
1582	31950	В	1607	I .	1440	
1583	31951	В	1608	1	1878	
1584	31952	С	1609	402	563	
1585	31953	В	1610	1	2964	
1586	31954	В	1611	1	1284	
1587	31955	C	1612	144	449	
1588	31956	В	1613	1	1050	
1589	31957	В	1614	1	561	
1590	31958	В	1615	127	330	
1591	31959	С	1616	202	443	
1592	31960	В	1617	l	924	
1593	31961	C	1618	60	419	
1594	31962	С	1619	285	602	
1595	31963	C	1620	1	93	
1596	31964	В	1621	1	480	
1597	31965	В	1622	96	416	·
1598	31966	В	1623	78	1581	
1599	31967	В	1624	1	2259	
1600	31968	С	1625	180	371	
1601	31969	В	1626	1	852	
1602	31970	В	1627	1	204	
1603	31971	В	1628	37	2613	
1604	31972	В	1629	66	1505	
1605	31973	В	1630	1	1792	
1606	31974	В	1631	100	522	
1607	31975	В	1632	252	2347	
1608	31976	С	1633	294	450	
1609	31977	С	1634	118	372	
1610	31978	В	1635	1	799	
1611	31979	В	1636	1	2496	
1612	31980	В	1637	100	1188	
1613	31981	В	1638	35	1654	
1614	31982	В	1639	46	783	
1615	31983	В	1640	8	1428	
1616	31984	В	1641	1	2121	
1617	31985	В	1642	92	667	
1618	31986	В	1643	1	339	
1619	31987	c	1644	79	434	
1620	31988	C	1645	592	921	
1621	31989	c	1646	1	171	
1622	31990	č	1647	76	264	
1623	31991	В	1648	157	912	
1624	31992	В	1649	10	462	
1625	31993	C	1650	10	333	
1626	31994	c	1651	763	1001	
1627	31995	В	1652	202	701	
1628	31996	C	1653	215	572	
1629	31997	В	1654	261	399	
1630	31997	С	1655	623	749	
1631	31998	В	1656	198	1524	
1632	32000	В	1657	108	575	
1032	32000	P _	1037	100	313	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				
1633	32001	В	1658	40	2173	
1634	32002	В	1659	1	479	
1635	32003	В	1660	1	1542	
1636	32004	В	1661	1	849	
1637	32005	В	1662	1	684	
1638	32006	В	1663	1	318	
1639	32007	В	1664	1	406	
1640	32008	В	1665	1	393	
1641	32009	В	1666	1	210	
1642	32010	В	1667	1	450	
1643	32011	В	1668	1	471	
1644	32012	В	1669	1	471	
1645	32013	В	1670	282	580	
1646	32014	В	1671	1	789	
1647	32015	В	1672	1	324	
1648	32016	В	1673	1	465	
1649	32017	В	1674	1	948	
1650	32018	c	1675	24	401	
1651	32019	В	1676	46	401	
1652	32020	В	1677	251	1041	
1653	32021	c	1678	1	177	
1654	32022	В	1679	i	189	
1655	32023	В	1680	65	769	
1656	32023	C	1681	1	564	
1657	32025	В	1682	65	769	
1658	32025	В	1683	1	1743	
1659	32026	В	1684	1	615	
		В		1	323	
1660	32028 32029	В	1685	1	618	
1661			1687	1	579	
	32030	B			216	
1663	32031	1	1688	142		
1664	32032	С	1689	145	432	
1665	32033	В	1690	1	729	
1666	32034	С	1691	1	192	
1667	32035	С	1692	1	474	
1668	32036	В	1693	326	1662	
1669	32037	В	1694	50	1462	
1670	32038	С	1695	1	432	
1671	32039	В	1696	173	375	
1672	32040	В	1697	1	1917	
1673	32041	В	1698	57	365	
1674	32042	В	1699	78	1250	
1675	32043	В	1700	8	2210	
1676	32044	В	1701	1	474	
1677	32045	В	1702	47	879	
1678	32046	В	1703	1	465	
1679	32047	В	1704	65	473	
1680	32048	В	1705	89	1908	
1681	32049	c	1706	1	612	
1682	32050	c	1707	80	226	
1683	32051	В	1708	992	2023	
1.002	- 200				1	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
		l		ocquence.		
1684	32052	В	1709	1293	1497	
1685	32053	В	1710	29	1480	
1686	32054	С	1711	1664	2179	
1687	32055	В	1712	183	8544	
1688	32056	С	1713	60	472	
1689	32057	В	1714	202	735	
1690	32058	В	1715	532	661	
1691	32059	В	1716	1	453	
1692	32060	В	1717	24	320	
1693	32061	В	1718	59	583	
1694	32062	В	1719	1	369	
1695	32063	В	1720	51	204	
1696	32064	В	1721	318	849	
1697	32065	В	1722	1	597	
1698	32066	В	1723	1	325	
1699	32067	В	1724	1	675	
1700	32068	В	1725	1	631	
1701	32069	В	1726	1	1017	
1702	32070	В	1727	158	727	
1703	32071	В	1728	296	798	
1704	32072	В	1729	1 '	1128	
1705	32073	С	1730	237	356	
1706	32074	С	1731	393	519	
1707	32075	В	1732	1	6432	
1708	32076	В	1733	124	402	
1709	32077	В	1734	35	421	
1710	32078	С	1735	203	385	
1711	32079	В	1736	16	406	
1712	32080	В	1737	21	306	
1713	32081	В	1738	97	352	
1714	32082	В	1739	64	7164	
1715	32083	В	1740	553	1197	
1716	32084	В	1741	553	720	
1717	32085	В	1742	1	4029	
1718	32086	В	1743	63	422	
1719	32087	В	1744	342	451	
1720	32088	В	1745	1	1238	
1721	32089	В	1746	1	2393	
1722	32090	В	1747	1667	1833	
1723	32091	С	1748	33	287	
1724	32092	В	1749	1	469	
1725	32093	В	1750	75	166	
1726	32094	В	1751	120	756	
1727	32095	С	1752	1	1098	
1728	32096	В	1753	1	486	
1729	32097	C	1754	25	374	
1730	32098	c	1755	149	394	
1731	32099	В	1756	1	660	
1732	32100	В	1757	26	391	
1733	32101	В	1758	282	419	
1734	32102	В	1759	132	717	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	l	09/540,217	sequence	or permue sequence	deletion, (-possible unelconde insertion)
				,		
1735	32103	В	1760	127	698	
1736	32104	В	1761	56	549	
1737	32105	В	1762	325	2681	
1738	32106	С	1763	465	893	
1739	32107	С	1764	123	764	
1740	32108	В	1765	206	402	
1741	32109	В	1766	393	900	
1742	32110	С	1767	1	360	
1743	32111	В	1768	285	482	
1744	32112	В	1769	1	405	
1745	32113	C	1770	304	399	
1746	32114	В	1771	1	273	
1747	32115	В	1772	67	1464	
1748	32116	В	1773	1	1122	
1749	32117	В	1774	li	1185	
1750	32118	В	1775	44	145	
1751	32119	В	1776	1	1050	
1752	32120	В	1777	250	762	
1753	32121	В	1778	1	390	
1754	32122	В	1779	172	867	
1755	32123	В	1780	327	637	
1756	32124	В	1781	1	1101	
1757	32125	C	1782	10	216	
1758	32126	В	1783	i i	1449	
1759	32127	В	1784	i	402	
1760	32128	c	1785	134	418	
1761	32129	В	1786	1	417	
1762	32130	В	1787	1	384	
1763	32131	c	1788	i	738	
1764	32132	c	1789	68	280	
1765	32132	В	1790	101	327	
1766	32134	В	1791	1	1257	
1767	32135	C	1792	168	311	
1768	32136	В	1792	33	120	
1769	32137	C	1794	1	150	
1770	32138	c	1794	1	378	
	32138	C	1796	100	267	
1771		c	1797	100	318	
1772 1773	32140 32141	C	1797	1	429	
		C		194	379	
1774	32142	В	1799	194	363	
1775	32143	_				
1776	32144	В	1801	1	384	
1777	32145	В	1802	1	4462	
1778	32146	В	1803	235	425	
1779	32147	В	1804	8	1187	
1780	32148	В	1805]	480	
1781	32149	В	1806	1	240	
1782	32150	В	1807	1	891	
1783	32151	C	1808	1	366	
1784	32152	В	1809	376	776	
1785	32153	В	1810	304	876	

SEQ ID	ICEO ID NO.	134.4	SEQ ID NO:	Nucleotide	Nucleotide Idention of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	cudon for last amino acid	*=Stop codon, /=possible nuclcotide
110.	sequence	liiou	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	'		i .	sequence	' ' '	
1786	32154	В	1811	1	939	
1787	32155	В	1812	4	744	
1788	32156	В	1813	1	717	
1789	32157	С	1814	67	366	
1790	32158	В	1815	185	847	
1791	32159	С	1816	1	315	
1792	32160	В	1817	87	297	
1793	32161	В	1818	1	1190	
1794	32162	В	1819	1	848	
1795	32163	В	1820	934	1158	
1796	32164	C	1821	1	477	
1797	32165	C	1822	6	125	
1798	32166	В	1823	335	536	
1799	32167	В	1824	157	324	
1800	32168	С	1825	176	361	
1801	32169	С	1826	1	120	
1802	32170	С	1827	25	360	
1803	32171	С	1828	246	377	
1804	32172	С	1829	4782	5015	
1805	32173	В	1830	1105	3034	
1806	32174	В	1831	818	874	
1807	32175	С	1832	1	444	
1808	32176	В	1833	589	734	
1809	32177	В	1834	1	264	
1810	32178	В	1835	46	112	
1811	32179	В	1836	1	360	
1812	32180	В	1837	589	734	
1813	32181	В	1838	1	675	
1814	32182	В	1839	1	1194	
1815	32183	В	1840	121	880	
1816	32184	В	1841	35	853	
1817	32185	В	1842	1	426	
1818	32186	C	1843	1	252	
1819	32187	В	1844	1	323	
1820	32188	В	1845	1	789	
1821	32189	C	1846	337	1521	
1822	32190	c	1847	1	345	
1823	32191	В	1848	331	3385	
1824	32192	В	1849	1	1584	
1825	32193	В	1850	i	957	
1826	32194	В	1851	226	1794	
1827	32195	В	1852	52	594	
1828	32196	C	1853	1	615	
1829	32197	В	1854	1	318	
1830	32198	В	1855	297	450	
1831	32198	C	1856	87	404	
1832	32200	c	1857	1	171	
1833	32200	c	1858	1	171	
1834	32201	В	1859	34	831	
1835	32202	В	1860	1	1375	
1836	32204	В	1861	1	546	
1830	32204	P	1001	P	540	

SEQ ID	Tero in vo	154.4	SEQ ID NO:	Nucleatide	Newtontide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1.00	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1.			sequence		
	l	<u>L_</u>				
1837	32205	С	1862	36	182	
1838	32206	В	1863	392	1043	
1839	32207	В	1864	I	1283	
1840	32208	С	1865	283	591	
1841	32209	С	1866	97	108	
1842	32210	С	1867	25	250	
1843	32211	С	1868	142	448	
1844	32212	C	1869	1	576	
1845	32213	С	1870	1	396	
1846	32214	В	1871	1	885	
1847	32215	С	1872	321	848	
1848	32216	В	1873	82	871	
1849	32217	C	1874	1	723	
1850	32218	C	1875	1	426	
1851	32219	С	1876	624	803	
1852	32220	В	1877	1	588	
1853	32221	В	1878	39	58	
1854	32222	В	1879	1	1011	
1855	32223	В	1880	1	654	
1856	32224	С	1881	1	498	
1857	32225	С	1882	1	249	
1858	32226	С	1883	507	785	
1859	32227	С	1885	310	404	
1860	32228	В	1886	448	618	
1861	32229	В	1887	1	388	
1862	32230	В	1888	106	414	
1863	32231	В	1889	82	4206	
1864	32232	В	1890	1	240	
1865	32233	В	1891	1	324	
1866	32234	С	1892	243	447	
1867	32235	C	1893	139	228	
1868	32236	c	1894	61	300	
1869	32237	c	1895	271	429	
1870	32238	В	1896	545	1054	
1871	32239	В	1897	609	706	
1872	32240	В	1898	1	2521	
1873	32241	c	1899	152	517	
1874	32242	В	1900	217	313	
1875	32243	c	1901	86	193	
1876	32244	č	1902	29	271	
1877	32245	В	1903	1	522	
1878	32246	C	1904	37	225	
1879	32247	c	1905	84	308	
1880	32247	В	1906	36	1569	
1881	32249	В	1907	1	522	
1882	32250	C	1908	 	510	
1883	32251	В	1909	1	936	
1884	32252	c	1910	1	162	
1885	32253	c	1911	155	427	
1886	32254	В	1911	1	1282	
1887	32255	В	1912	165	270	
100/	34433	10	1713	1103	1270	

SEQ ID NO: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: Not Seq ID No: No: Not Seq ID No: No: No: No: No: No: No: No: No: No:	SEQ ID	ISEO ID NO:	Mat	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
sequence opstiguence sequence openation sequence sequence sequence deletion. possible nucleotide insertion) 1888 32255 B 1914 513 9470 1889 32257 B 1915 35 871 1890 32258 B 1916 1 690 1892 32260 C 1919 14 301 1894 32262 B 1918 1 690 1894 32262 B 1920 1 306 1895 32263 B 1922 36 238 1897 32265 B 1922 36 238 1897 32265 B 1922 36 238 1899 32267 C 1926 96 263 1899 32269 B 1927 1 207 1900							
Section Sect							
1889 32257 B 1915 35 871 1890 32258 B 1916 1 690 1891 32259 C 1917 86 271 1892 32260 B 1918 1 690 1894 32262 B 1919 14 301 1894 32262 B 1920 1 936 1895 32263 B 1921 1 1901 1896 32264 B 1922 36 238 1897 32265 B 1921 1 1901 1898 32266 C 1924 5 364 1899 32267 C 1925 43 494 1900 32268 C 1926 96 263 1901 32270 B 1927 1 207 1902 32271 B 1930 2271 408					sequence		
1889 32257 B 1915 35 871 1890 32258 B 1916 1 690 1891 32259 C 1917 86 271 1892 32260 B 1918 1 690 1894 32262 B 1919 14 301 1894 32262 B 1920 1 936 1895 32263 B 1921 1 1901 1896 32264 B 1922 36 238 1897 32265 B 1921 1 1901 1898 32266 C 1924 5 364 1899 32267 C 1925 43 494 1900 32268 C 1926 96 263 1901 32270 B 1927 1 207 1902 32271 B 1930 2271 408	1000	122256	I .	1014	1512	0470	
1890 32258 B 1916 1 690 690 1887 32259 C 1917 86 271 670							
1891 32259 C 1917 86 271 1892 32260 B 1918 1 690							
1892 32260 B 1918 I 900 900 1893 32261 C 1919 14 301 1894 32262 B 1920 I 936 936 1895 32263 B 1921 I 1901 1896 32264 B 1922 36 238 1897 32265 B 1923 I 738 1898 32266 C 1924 5 364 3							
1895 32261 C 1919 14 301							
1894 32262 B 1920 1 936							
1895 32263 B 1921 1 1991 1887 32265 B 1922 36 238 38 32266 C 1924 5 364 4 4 4 4 4 4 4 4 4							
1896 32264 B 1922 36 238 1898 1898 32265 C 1924 5 364 4 4 4 4 4 4 4 4 4							
1897 32265 B 1923 1 738 8 1898 32266 C 1924 5 364 4 4 4 4 4 4 4 4 4							
1898 32266 C 1924 5 364			-				
1899 32267 C 1925 43 494 494 1900 32268 C 1926 96 263 63 63 64 64 64 64 64							
1900 32268 C 1926 96 263							
1902 32270 B 1928 1 290							-
1903 32271 B 1929 52 482 1904 32273 B 1930 271 408 1906 32273 B 1931 114 309 1906 32273 B 1931 114 309 1906 32274 C 1932 218 398 1907 32275 B 1933 1 1011 111 1908 32276 B 1934 1 702 1909 32277 B 1935 1 1305 1909 32278 C 1936 141 374 1911 32279 B 1935 1 1305 1911 32278 C 1936 141 374 374 1911 32279 B 1937 1 834 4 1912 32280 B 1938 47 363 363 1912 32280 B 1938 47 363 364 1915 32281 B 1940 373 558 1914 32282 B 1940 373 558 1917 1 1918 32283 B 1941 96 377 1916 32284 B 1942 55 2711 1917 32285 B 1945 833 1352 1918 32286 B 1946 1 1101 1919 32287 B 1947 865 1070 1920 32288 C 1948 1 285 1070 1922 32290 B 1950 124 813 1922 32290 B 1950 124 813 1922 32290 B 1950 124 813 1922 32290 B 1950 124 813 1923 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 32290 B 1950 124 813 1924 3229 B 1957 1 678 1926 3229 B 1957 1 678 1926 3229 B 1957 1 675 1926 3229 B 1950 124 325 326 326 B 1964 1 71 251 1934 3230 B 1064 1 71 251 1934 3230 B 1065 117 1109 1009 1000							
1904 32272 B 1930 271 408 1905 32273 B 1931 114 309 309 309 309 32274 C 1932 218 398 398 393 1 1011 32275 B 1934 1 702 32275 B 1934 1 702 32275 B 1935 1 1305 32276 C 1936 141 374 3							
1905 32273 B 1931 114 309 32274 C 1932 218 398 398 3275 B 1933 1 1011 1011 1011 1019 32275 B 1933 1 1011 1 702 1090 32276 B 1934 1 702 7							
1906 32274 C 1932 218 398 1907 32275 B 1933 1 1011 1019 1019 32276 B 1934 1 702 102 1019 102							
1907 32275 B 1933 1 1011 1011 10908 32276 B 1934 1 702 702 703 703 704 705 7							
1908 32276 B 1934 1 702 1909 32277 B 1935 1 1305 1909 32277 B 1935 1 1305 1910 32278 C 1936 141 374 374 374 32280 B 1937 1 834 4 363 32280 B 1937 1 834 4 363 32280 B 1937 1 834 4 363 32280 B 1939 73 558 32281 B 1940 373 864 4 3282 B 1940 373 864 4 32282 B 1940 373 864 4 32282 B 1941 96 377 374 375 3							
1909 32277 B 1925 1 1305 3278 C 1936 141 374 374 374 374 374 374 374 374 374 374 375 3229 B 1937 1 834 363 374 375 3281 B 1938 47 363 363 377 375 375 375 377							
1910 32278 C 1936 141 374 374 32279 B 1937 1 834 34 34 34 34 34 34 3							
1911 32279 B 1937 1 834 1912 32280 B 1938 47 363 1913 32281 B 1939 73 558 1914 32382 B 1940 373 864 1915 32283 B 1940 373 864 1916 32284 B 1942 55 2711 1916 32284 B 1942 55 2711 1917 32285 B 1945 833 1352 1918 32286 B 1946 1 1101 1919 32287 B 1947 865 1070 1920 32288 C 1948 1 285 1921 32289 B 1949 1 642 1922 32290 B 1950 124 813 1923 32291 B 1951 1 654 1924 32292 B 1951 1 654 1924 32292 B 1955 100 303 1925 32294 B 1951 1 654 1926 32294 B 1955 100 824 1928 32295 C 1955 52 348 1929 32297 B 1957 1 678 1928 32298 B 1957 1 678 1928 32296 C 1956 52 348 1930 32298 B 1959 1 675 1931 32299 B 1959 1 675 1931 32299 B 1950 124 348 1933 32301 B 1961 71 251 1934 32303 B 1963 1 453 1937 32303 B 1964 1 375 1937 32305 B 1965 117 1109							
1913 32281 B 1939 73 558			В		47	363	
1914 32282 B 1940 373 864							
1915 32283 B 1941 96 377 1916 32284 B 1942 55 2711 1917 32285 B 1945 833 1352 3285 B 1946 1 1101 1919 32287 B 1946 1 1101 1919 32287 B 1947 865 1070 32288 C 1948 1 285 32286 C 1948 1 285 32290 B 1950 124 813 32290 B 1950 124 813 32291 8292 B 1951 1 654 6			В	1940	373	864	
1916 32284 B 1942 55 2711			В			377	
1917 32285 B 1945 833 1352			В	1942	55	2711	
1918 32286 B 1946 1 1101 1101 1919 32287 B 1947 865 1070 1920 32288 C 1948 1 285 1070 1921 32289 B 1947 865 1070 1921 32289 B 1949 1 642 1922 32290 B 1950 124 813 1923 32291 B 1951 1 654 4 1924 32292 B 1952 180 303 1924 32292 B 1953 15 170 1926 32294 B 1953 15 170 1926 32294 B 1954 245 646 6 1927 32295 B 1955 100 824 1928 32296 C 1956 52 348 1929 32297 B 1957 1 678 1929 32297 B 1957 1 678 1930 32298 B 1958 1 954 1951 32299 B 1959 1 675 1933 32299 B 1959 1 675 1933 32291 B 1960 52 348 1933 32291 B 1961 71 251 1934 3229 B 1962 427 747 1935 32303 B 1963 1 453 1934 32304 B 1964 1 375 1937 337 3380 B 1964 1 375 1937 337 3380 B 1964 1 375 1937 337 337 8 1964 1 375 1937 337 337 8 1965 117 1109 100		32285	В	1945	833	1352	-
1920 32288 C 1948 1 285			В	1946	1		
1921 32289 B 1949 1 642 813 1923 32290 B 1950 124 813 1950 124 813 1950 124 813 1954 125 180 1924 180 1925 32292 B 1951 1 654 1925 32293 C 1953 15 170 1926 32294 B 1954 245 646 1927 32295 B 1955 100 824 1928 32296 C 1956 52 348 1928 32297 B 1957 1 678 1930 32298 B 1958 1 954 4 1931 32295 B 1956 100 824 1929 32297 B 1957 1 678 1930 32298 B 1958 1 954 1931 32299 B 1959 1 675 1931 32299 B 1958 1 954 1931 32299 B 1958 1 954 1931 32299 B 1958 1 954 1931 32299 B 1958 1 954 1931 3230 B 1961 71 251 1934 3230 B 1961 71 251 1934 3230 B 1963 1 453 1953 3230 B 1963 1 453 1957 1937 32305 B 1965 117 1109	1919	32287	В	1947	865	1070	
1922 32290 B 1950 124 813	1920	32288	c	1948	1	285	
1923 32291 B 1951 1 654	1921	32289	В	1949	1	642	
1924 32292 B 1952 180 303	1922	32290	В	1950	124	813	
1925 32293 C 1953 15 170 1926 32294 B 1954 245 646 1927 32295 B 1955 100 824 1928 32296 C 1956 52 348 1929 32297 B 1957 1 678 1930 32298 B 1958 1 954 1931 32299 B 1957 1 675 1932 32300 C 1960 52 348 1932 32300 C 1960 52 348 1933 32301 B 1961 71 251 1934 32302 B 1962 427 747 1935 32303 B 1963 1 453 1937 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1923	32291	В	1951	1	654	
1926 32294 B 1954 245 646	1924	32292	В	1952	180	303	
1927 32295 B 1955 100 824	1925	32293	С	1953	15	170	
1928 32296 C 1956 52 348 1929 32297 B 1957 1 678 1930 32298 B 1958 1 954 1931 32299 B 1959 1 675 1932 32300 C 1960 52 348 1933 32301 B 1961 71 251 1934 32302 B 1962 427 747 1936 32304 B 1963 1 453 1936 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1926	32294	В	1954	245	646	
1929 32297 B 1957 1 678 1930 32298 B 1958 1 954 1931 32299 B 1959 1 675 1932 23200 C 1960 52 348 1933 32301 B 1961 71 251 1934 23302 B 1962 427 747 1935 32303 B 1963 1 453 1936 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1927	32295	В	1955	100	824	
1930 32298 B 1958 1 954 1931 32299 B 1959 1 675 1952 32300 C 1960 52 348 1933 32301 B 1961 71 251 1934 32302 B 1962 427 747 1935 32303 B 1963 1 453 1936 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1928	32296	С	1956	52	348	
	1929	32297	В	1957	1	678	
1932 32300 C 1960 52 348 1933 32301 B 1961 71 251 1934 32302 B 1962 427 747 1935 32303 B 1963 1 453 1936 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1930	32298	В	1958	1	954	
1933 32301 B 1961 71 251 1934 32302 B 1962 427 747 1935 32303 B 1963 1 453 1936 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1931	32299	В	1959	1	675	
1934 32302 B 1962 427 747 1935 32303 B 1963 1 453 1936 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1932	32300	С	1960	52	348	
1935 32303 B 1963 1 453 1936 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1933	32301	В	1961	71	251	
1936 32304 B 1964 1 375 1937 32305 B 1965 117 1109	1934	32302	В		427		
1937 32305 B 1965 117 1109					1		
	1936	32304			1		
1938 32306 C 1966 47 133							
	1938	32306	С	1966	47	133	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		L		sequence		
1939	32307	В	1967	79	1149	
1940	32308	В	1968	1	693	
1941	32309	В	1969	1	1179	
1942	32310	В	1970	1	639	
1943	32311	В	1971	502	1294	
1944	32312	С	1972	670	1185	
1945	32313	В	1973	1	1044	
1946	32314	В	1974	1 .	3645	
1947	32315	В	1975	1	2877	
1948	32316	В	1976	1	1579	
1949	32317	В	1977	1	750	
1950	32318	В	1978	1	438	
1951	32319	С	1979	122	307	
1952	32320	С	1980	71	271	
1953	32321	С	1981	151	363	
1954	32322	С	1982	122	307	
1955	32323	С	1983	55	282	
1956	32324	С	1984	89	385	•
1957	32325	С	1985	48	275	
1958	32326	С	1986	246	557	
1959	32327	В	1987	394	2565	
1960	32328	В	1988	1	432	
1961	32329	В	1989	46	483	
1962	32330	В	1990	150	482	
1963	32331	В	1991	10	265	
1964	32332	С	1992	40	162	
1965	32333	В	1993	1	3639	
1966	32334	В	1994	83	179	
1967	32335	В	1995	39	1452	
1968	32336	В	1996	50	384	
1969	32337	В	1997	256	351	
1970	32338	В	1998	1	771	
1971	32339	В	1999	1	489	
1972	32340	В	2000	37	447	•
1973	32341	В	2001	1	1272	
1974	32342	В	2002	1	2559	
1975	32343	С	2003	221	589	
1976	32344	С	2004	415	1033	
1977	32345	В	2007	318	694	
1978	32346	B_	2008	31	819	
1979	32347	В	2009	1	276	
1980	32348	В	2010	1	369	
1981	32349	В	2011	85	628	
1982	32350	В	2012	19	178	
1983	32351	В	2013	217	393	
1984	32352	В	2014	1	779	
1985	32353	В	2015	107	650	
1986	32354	В	2016	313	527	
1987	32355	В	2017	32	258	
1988	32356	С	2018	51	345	
1989	32357	В	2019	1	393	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1990	32358	В	2020	647	1362	
1991	32359	C	2021	16	378	
1992	32360	В	2022	32	349	
1993	32361	c	2023	256	425	
1994	32362	c	2024	134	382	
1995	32363	В	2025	138	171	
1996	32364	В	2026	1	1626	
1997	32365	В	2027	509	810	
1998	32366	c	2028	1	513	
1999	32367	c	2029	7	375	
2000	32368	c	2030	1	410	
2001	32369	В	2031	i	864	
2002	32370	В	2032	110	928	
2003	32371	В	2033	1	1026	
2004	32372	В	2034	1	1008	
2005	32373	В	2035	1	588	
2005	32374	В	2036	1	412	
2007	32375	В	2037	1	1851	
2008	32376	В	2038	309	663	
2009	32377	В	2039	1	525	
2010	32378	В	2040	1	2214	
2011	32379	В	2041	1	486	•
2012	32379	В	2041	1	774	
2012	32380	В	2042	1	596	
2013	32382	В	2043	305	395	
2014	32382	C	2044	27	185	
2015	32384	В	2045	1	1071	
2017	32385	В	2046	1	1326	
2017	32386	В	2047	1	3761	
2018	32380	C	2048	55	189	
2020		В	2049	1016	1683	
2020	32388	C	2050	942		
	32389	-	2052		1130	
2022	32390	В		1	598	
2023	32391	В	2053	1	768 999	
2024	32392	_	2054	1		
2025	32393	C	2055	1	252	
2026	32394	B B	2056	154	606	
2027	32395	_	2057	1	846	
2028	32396	С		334	690	
2029	32397	В	2059	268	5712	
2030	32398	С	2060	117	662	
2031	32399	В	2061	1	3504	
2032	32400	В	2062	816	927	
2033	32401	В	2063	1	342	
2034	32402	В	2064	1	1443	
2035	32403	С	2065	53	102	
2036	32404	С	2066	271	528	
2037	32405	В	2067	1	843	
2038	32406	С	2068	187	408	
2039	32407	С	2069	174	320	
2040	32408	В	2070	31	534	

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SEO ID	lero ID NO.	Taxa.	SEQ ID NO:	Nucleutida	Talustantide legation of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop cudon, /=possible nucleotide
1.01	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \spossible nucleotide insertion)
		1		sequence		· ·
		10	I a a m .	1.00	1.20	
2041	32409	С	2071	183	329	
2042	32410	В	2072	3	389	
2043	32411	В	2073	78	974	
2044	32412	В	2074	467	692	
2045	32413	C	2075	605	965	
2046	32414	В	2076	1	555	
2047	32415	В	2077	1	390	
2048	32416	В	2078	1	2522	
2049	32417	В	2079	24	94	
2050	32418	В	2080	78	593	
2051	32419	В	2081	1	612	
2052	32420	В	2082	42	342	
2053	32421	В	2083	ì	477	
2054	32422	В	2084	57	1640	
2055	32423	С	2085	110	307	
2056	32424	В	2086	1	591	
2057	32425	С	2087	14	355	
2058	32426	В	2088	47	998	
2059	32427	В	2089	1	498	
2060	32428	С	2090	357	560	
2061	32429	В	2091	1	522	
2062	32430	С	2092	231	659	
2063	32431	С	2093	36	167	
2064	32432	В	2094	394	2695	
2065	32433	В	2096	61	2215	
2066	32434	В	2097	204	572	
2067	32435	C	2098	476	652	
2068	32436	В	2099	1	190	
2069	32437	С	2100	1	259	
2070	32438	В	2101	1	2625	
2071	32439	В	2102	1403	2950	
2072	32440	В	2103	672	1955	
2073	32441	С	2104	ł	351	
2074	32442	В	2105	1	567	
2075	32443	С	2106	176	304	
2076	32444	С	2107	27	308	
2077	32445	С	2108	68	307	
2078	32446	C	2109	322	567	-
2079	32447	В	2110	1	1297	
2080	32448	В	2111	281	1488	
2081	32449	В	2112	12	2497	
2082	32450	c	2113	90	284	
2083	32451	В	2114	1	2466	
2084	32452	В	2115	1	603	
2085	32453	В	2116	1	954	
2086	32454	В	2117	205	441	
2087	32455	В	2118	68	2052	
2088	32456	В	2119	271	639	
2089	32457	В	2120	1	1356	
2090	32458	В	2121	247	1326	
2091	32459	В	2122	1	1041	
_	1					

SEQ ID	SEQ ID NO:	Tates	SEQ ID NO:	Nucleatide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
2092	32460	В	2123	1	1695	
2092	32461	В	2124	1	1767	
2093	32462	В	2124	1	2286	
2094	32463	В	2126	1	1167	
2093	32464	В	2127	1	2343	
2090	32465	В	2128	1	1056	
2097	32466	В	2128	1	1379	
2099	32467	В	2130	1	1839	
2100	32467	В	2131	1	5460	
		В	2132	133	549	
2101	32469 32470	В	2132	1	534	
				<u> </u>		
2103	32471	В	2134	1	537	
2104	32472	В	2135	1		
2105	32473	C	2136	1	432	
2106	32474	В	2137	1	615	
2107	32475	В	2138	146	556	
2108	32476	В	2139	133	1434	
2109	32477	В	2140	1	357	
2110	32478	С	2141	1	429	
2111	32479	В	2142	1	411	
2112	32480	В	2143	1	459	
2113	32481	С	2144	224	550	
2114	32482	В	2145	1	1035	
2115	32483	В	2146	1	342	
2116	32484	С	2147	1	321	
2117	32485	С	2148	1	317	
2118	32486	В	2149	1	495	
2119	32487	В	2150	146	556	
2120	32488	С	2151	1	390	
2121	32489	С	2152	461	643	
2122	32490	С	2153	198	416	
2123	32491	С	2154	258	500	
2124	32492	В	2155	291	1034	
2125	32493	В	2156	1	834	
2126	32494	В	2157	1	7852	
2127	32495	В	2158	1	1320	
2128	32496	В	2159	1631	1756	
2129	32497	В	2160	500	8643	
2130	32498	С	2161	193	475	
2131	32499	В	2162	1	795	
2132	32500	В	2163	1	663	
2133	32501	С	2164	1	303	
2134	32502	В	2165	266	385	
2135	32503	В	2166	1	704	
2136	32504	В	2167	1	720	
2137	32505	В	2168	364	507	
2138	32506	В	2169	44	197	
2139	32507	С	2170	72	224	
2140	32508	С	2171	228	393	
2141	32509	С	2172	241	396	
2142	32510	С	2173	415	552	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
2143	32511	В	2174	64	268	
2144	32512	C	2175	1	462	
2144	32512	C	2176	1	357	
2146	32514	В	2177	1	3213	
2147	32514	В	2178	119	682	
2148	32516	В	2179	119	405	
2149	32517	В	2180	297	769	
2150	32518	В	2181	1	1314	
2151	32519	C	2182	156	287	
2152	32520	В	2183	1	756	
2153	32521	В	2184	<u> </u>	645	
2154	32522	В	2185	li -	948	
2155	32523	В	2186	<u> </u>	660	
2156	32524	В	2187	186	518	
2157	32525	В	2188	1	3570	
2158	32526	В	2189	1	3354	
2159	32527	В	2190	1	2232	
2160	32528	В	2191	1	1356	
2161	32529	В	2192	i	1103	
2162	32530	В	2192	li li	1902	
2163	32531	В	2193	1	2232	
2164	32532	В	2194	1	2991	
2165	32533	В	2195	1	2136	
2166	32534	В	2190	1	1524	
2167	32535	В	2197	1	2106	
2168	32536	В	2199	1	1224	
2169	32537	В	2200	1	1935	
2170	32538	В	2201	1	1428	
2171	32539	В	2202	1	858	
2172	32540	В	2202	 	2162	
2172	32541	В	2203	1	1374	
2173	32542	В	2204	205	3666	
2175	32543	В	2206	59	4311	
2176	32544	В	2207	1	1311	
2177	32545	В	2208	1	2742	
2178	32546	В	2209	1	1878	
2179	32547	В	2210	1	1074	
2180	32548	В	2211	<u> </u>	2217	
2181	32549	В	2212	'	1945	
2182	32550	В	2212	1	1941	
2183	32551	В	2214	1	1737	
2184	32552	В	2214	1	1422	
2184	32553	В	2216	22	9087	
2186	32553	В	2217	1	4954	
2180	32555	В	2218	 	1812	
2188		B B	2218	1	939	
	32556	_		-		
2189	32557	В	2220	1	2895	
2190 2191	32558	В	2221		6223	
2191	32559	В	2222	109 3807	4966 9479	
	32560	В				
2193	32561	В	2224	1	4903	

SEQ ID	ICEO ID NO.	Mari	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
2194	120562	<u> </u>	2225	1210	516	
	32562 32563	B	2226	210	516 292	
2195		_	2227			
2196	32564 32565	В	2228	1	657	
			2228			
2198	32566 32567	B C	2230	69	1303	
2200	32568	В	2231	1	321	
2200	32569	В	2232	88	522	
2202	32570	В	2232	527	1207	
2202	32570	В	2234	118	375	
2203	32572	В	2234	8	148	
2205	32573	В	2236	609	1121	
2206	32574	В	2237	1	1500	
2207	32575	C	2238	121	330	
2208	32576	В	2239	1	591	
2209	32577	В	2240	125	471	
2210	32578	В	2240	64	909	
2211	32579	В	2242	13	579	
2212	32580	В	2242	249	531	
2212	32581	c	2244	107	928	
2214	32582	В	2245	213	322	
2215	32583	C	2246	373	441	
2216	32584	В	2247	54	2723	
2217	32585	В	2248	94	529	***
2218	32586	В	2249	57	260	
2219	32587	В	2250	674	1972	
2220	32588	В	2251	1	1053	
2221	32589	c	2252	186	347	
2222	32590	В	2253	26	193	
2223	32591	В	2254	1	5442	
2224	32592	В	2255	428	3792	
2225	32593	В	2256	9	199	
2226	32594	В	2257	421	2932	
2227	32595	В	2258	305	547	
2228	32596	В	2259	1	891	
2229	32597	В	2260	1	641	
2230	32598	В	2261	108	542	
2231	32599	В	2262	105	440	
2232	32600	В	2263	553	729	
2233	32601	В	2264	1	645	
2234	32602	В	2265	291	452	
2235	32603	В	2266	143	348	
2236	32604	С	2267	310	426	
2237	32605	В	2268	1	1344	
2238	32606	В	2269	237	2834	
2239	32607	В	2270	1	2922	
2240	32608	В	2271	109	3499	
2241	32609	В	2272	1	1611	
2242	32610	В	2273	1	1575	
2243	32611	В	2274	1	1314	
2244	32612	В	2275	1	1209	

SEQ ID	lero in vo.	Dist	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.0.	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1	ļ ·	1		sequence	,	
2245	32613	В	2276	1	2022	
2246	32614	В	2277	1	1938	
2247	32615	В	2279	1	1806	
2248	32616	В	2280	I	2361	
2249	32617	В	2281	1	2732	
2250	32618	В	2282	l	3703	
2251	32619	C	2283	1	507	
2252	32620	В	2284	118	316	
2253	32621	В	2285	1	272	
2254	32622	В	2286	37	388	
2255	32623	В	2287	1_	660	
2256	32624	В	2288	431	633	
2257	32625	В	2289	1	1032	
2258	32626	В	2290	1	1227	
2259	32627	С	2291	27	296	
2260	32628	В	2292	58	370	
2261	32629	В	2293	1	1275	
2262	32630	В	2294	1	1299	
2263	32631	С	2295	227	613	
2264	32632	В	2296	1	297	
2265	32633	В	2297	126	206	
2266	32634	С	2298	1	387	
2267	32635	В	2299	19	279	
2268	32636	В	2300	1	612	
2269	32637	С	2301	81	191	
2270	32638	В	2302	120	308	
2271	32639	В	2303	1	2145	
2272	32640	С	2304	270	416	
2273	32641	В	2305	31	627	
2274	32642	В	2306	128	499	
2275	32643	В	2307	61	388	
2276	32644	В	2308	744	2094	
2277	32645	В	2309	241	669	
2278	32646	В	2310	1	285	
2279	32647	В	2311	137	307	
2280	32648	С	2312	168	362	
2281	32649	С	2313	8	394	
2282	32650	В	2314	1	489	
2283	32651	С	2315	1	204	
2284	32652	В	2316	1	2361	
2285	32653	В	2317	1	2265	
2286	32654	В	2318	i	2268	
2287	32655	В	2319	1	2337	
2288	32656	В	2320	i	2196	
2289	32657	В	2321	1	2298	
2290	32658	В	2322	1	2880	
2291	32659	В	2323	1	2562	
2292	32660	В	2324	1	2835	
2293	32661	В	2325	1	2172	
2294	32662	В	2326	675	2515	
2295	32663	В	2327	1	2709	
4273	152005	Ľ_	2021	ı <u>. </u>	2,00	

SEQ ID	ISEO ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	coden for last amine acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	l			sequence		
2296	32664	В	2328	l 	2478	
2297	32665	В	2329	1	2748	
2298	32666	В	2330	877	4763	
2299	32667	В	2331	1	2590	
2300	32668	В	2332	1	597	
2301	32669	С	2333	279	412	
2302	32670	С	2334	507	878	
2302	32671	c	2335	1	147	
2304	32672	В	2336	52	573	
2304	32673	C	2337	211	446	
2306	32674	В	2338	1	1669	
2307	32675	В	2339	69	418	
2307	32676	В	2340	1	2778	
		В	2340	1	1896	
2309	32677	-	2341		1836	
2310	32678 32679	B B	2342	1	2463	
		В	2344	287	1785	
2312	32680				2860	
2313	32681	В	2345	1		
2314	32682	В	2346	1	1281	
2315	32683	В	2347	1	1176	
2316	32684	В	2348	1	1431	
2317	32685	В	2349	1	2361	
2318	32686	В	2350	592	1815	
2319	32687	В	2351	1	2764	
2320	32688	С	2352	309	581	
2321	32689	В	2353	99	5619	
2322	32690	В	2354	133	3213	
2323	32691	В	2355	1	3193	
2324	32692	В	2356	1	3291	
2325	32693	В	2357	1	4019	
2326	32694	В	2358	167	4093	
2327	32695	В	2359	1	3534	
2328	32696	В	2360	1	3405	
2329	32697	В	2361	1	3555	
2330	32698	В	2362	1	3786	
2331	32699	В	2363	1	3414	
2332	32700	В	2364	1	5130	
2333	32701	В	2365	1	8244	
2334	32702	В	2366	1	7995	
2335	32703	В	2367	1	1980	
2336	32704	В	2368	1	4269	
2337	32705	В	2369	1	169	
2338	32706	В	2370	1	573	
2339	32707	В	2371	388	1101	
2340	32708	С	2372	1	354	
2341	32709	В	2373	134	1057	
2342	32710	В	2374	91	1464	
2343	32711	В	2375	117	767	
2344	32712	В	2376	1	486	
2345	32713	С	2377	1	726	
2346	32714	С	2378	31	447	

SEQ ID	SEQ ID NO:	Met		Nucleotide		Amino acid sequence (X=Unknown,
NÒ:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
2347	32715	В	2379	1	402	
2348	32716	В	2380	22	427	
2349	32717	В	2381	351	560	~~~
2350	32718	В	2382	1	1122	
2351	32719	В	2383	1	1035	
2352	32720	В	2384	1	309	
2353	32721	В	2385	80	673	
2354	32722	В	2386	160	659	
2355	32723	В	2387	1	858	
2356	32724	C	2388	228	365	
2357	32725	В	2389	ı	531	
2358	32726	В	2390	218	670	
2359	32727	C	2391	182	484	
2360	32728	С	2392	1	738	
2361	32729	c	2393	27	316	
2362	32730	В	2394	291	498	
2363	32731	C	2395	230	409	
2364	32732	В	2396	228	1361	
2365	32733	c	2397	210	548	
2366	32734	В	2398	309	1202	
2367	32735	c	2399	100	406	
2368	32736	В	2400	440	2579	
2369	32737	C	2401	102	359	
2370	32738	В	2402	1	414	
2371	32739	В	2403	717	976	
2372	32740	В	2404	ī	777	
2373	32741	В	2405	1	208	
2374	32742	В	2406	ī	570	
2375	32743	В	2407	187	525	
2376	32744	В	2408	20	499	
2377	32745	В	2409	ī	210	
2378	32746	В	2410	41	166	
2379	32747	В	2411	29	348	
2380	32748	В	2412	ī	564	
2381	32749	C	2413	250	366	
2382	32750	В	2414	164	430	
2383	32751	С	2415	141	340	
2384	32752	В	2416	304	422	
2385	32753	В	2417	1	2031	-
2386	32754	В	2418	1 .	1527	
2387	32755	В	2419	i	2892	
2388	32756	В	2420	218	4186	
2389	32757	В	2421	203	655	
2390	32758	C	2422	1	346	
2391	32759	В	2423	299	433	
2392	32760	В	2424	172	525	
2392	32761	В	2425	1	3270	
2393	32762	В	2426	202	481	
2394	32762	В	2427	148	3473	
2396	32764	C	2428	182	460	
2396	32765	В	2429	116	2953	
14371	124103	10	6467	1110		ı

SEQ ID	ISEO ID NO:	TMet	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
	L	<u> </u>				
2398	32766	В	2430	153	332	
2399	32767	В	2431	267	2752	
2400	32768	В	2432	1	848	
2401	32769	С	2433	54	350	
2402	32770	В	2434	160	531	
2403	32771	В	2435	159	184	
2404	32772	В	2436	44	293	
2405	32773	С	2437	129	438	
2406	32774	С	2438	255	469	
2407	32775	В	2439	292	456	
2408	32776	В	2440	86	225	
2409	32777	В	2441	1	603	
2410	32778	В	2442	305	402	
2411	32779	С	2443	117	332	
2412	32780	В	2444	1	642	
2413	32781	В	2445	50	238	
2414	32782	В	2446	350	1331	
2415	32783	В	2447	1	867	
2416	32784	В	2448	1	498	
2417	32785	В	2449	40	849	
2418	32786	В	2450	187	404	
2419	32787	В	2451	1	921	
2420	32788	В	2452	439	517	
2421	32789	С	2453	143	682	
2422	32790	В	2454	87	401	
2423	32791	В	2455	44	277	
2424	32792	В	2456	1	639	
2425	32793	В	2457	1	816	
2426	32794	В	2458	100	454	
2427	32795	С	2459	717	923	
2428	32796	c	2460	1	412	
2429	32797	c	2461	80	394	
2430	32798	В	2462	278	323	
2431	32799	c	2463	9	239	
2432	32800	В	2464	1	537	
2433	32801	В	2465	1	798	
2434	32802	В	2466	1	861	
2435	32803	В	2467	611	979	
2436	32804	В	2468	56	166	
2437	32805	c	2469	40	495	
2438	32806	В	2470	1	216	
2439	32807	В	2471	273	385	
2440	32808	В	2472	77	489	
2441	32809	c	2473	480	791	
2442	32810	В	2474	110	1318	
2443	32811	В	2475	114	563	
2444	32812	В	2476	813	3193	
2445	32813	С	2477	198	650	
2445	32814	В	2477	198	234	
2447	32815	В	2479	7	174	
2447	32816	В	2480	1	1035	
2440	122010	10_	2700	1'	1000	

SEO ID	SEQ ID NO:	INC.	SEQ ID NO:	Nucleotide	TNustratide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	endon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	""	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
2449	32817	В	2481	1	564	
2450	32818	В	2482	16	894	
2451	32819	В	2483	1	207	
2452	32820	В	2484	1	2742	
2453	32821	В	2485	1	1071	
2454	32822	В	2486	58	1228	
2455	32823	C	2487	51	179	
2456	32824	В	2488	1	1119	
2457	32825	С	2489	147	398	
2458	32826	С	2490	1	504	
2459	32827	C	2491	4	240	
2460	32828	В	2492	190	388	
2461	32829	В	2493	1	594	
2462	32830	c	2494	299	477	
2463	32831	В	2495	1	2328	
2464	32832	C	2496	1	924	
2465	32833	В	2497	1	2703	
2466	32834	В	2498	504	1392	
2467	32835	lc	2499	649	1239	
2468	32836	В	2500	46	842	
2469	32837	В	2501	251	555	1 1
2470	32838	В	2502	258	326	
2471	32839	В	2503	49	386	
2472	32840	c	2504	63	383	
2473	32841	В	2505	150	585	
2474	32842	В	2506	65	678	
2475	32843	C	2507	477	634	
2476	32844	В	2508	80	337	
2477	32845	В	2509	1	1233	
2478	32846	В	2510	i	2526	
2479	32847	В	2511	192	2617	
2480	32848	В	2512	1	921	
2481	32849	В	2513	i	1650	
2482	32850	В	2514	79	1587	
2483	32851	В	2515	1	657	
2484	32852	В	2516	i	1260	
2485	32853	В	2517	i	762	
2486	32854	C	2518	1	729	
2487	32855	В	2519	1	1299	
2488	32856	В	2520	1	882	
2489	32857	C	2521	1	369	
2489			2522		573	
	32858	В		52	570	
2491	32859	В	2523	1		
2492	32860	В	2524	1	2376	
2493	32861	В	2525	1	786	
2494	32862	В	2526	1	760	
2495	32863	В	2527	73	714	
2496	32864	В	2528	1	2976	
2497	32865	В	2529	1	1021	
2498	32866	В	2530	1	1386	
2499	32867	В	2531	352	1239	

SEO ID	SEO ID NO	Tates	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /-possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	1	
2500	32868	В	2532	lt .	1740	
2501	32869	В	2533	li	915	
2502	32870	В	2534	392	1393	
2503	32871	В	2535	1	4868	
2504	32872	В	2536	i	2667	
2505	32873	В	2537	ti -	825	
2506	32874	В	2538	i	735	
2507	32875	В	2539	88	469	
2508	32876	c	2540	1	390	
2509	32877	c	2541	113	328	
2510	32878	B	2542	475	848	
2511	32879	В	2543	472	1482	
2512	32880	c	2544	42	593	
2513	32881	B	2545	470	998	
2514	32882	В	2546	83	339	
2515	32883	В	2547	1	501	
2516	32884	В	2548	1198	1432	
2517	32885	В	2549	1	486	
2518	32886	В	2550	454	1626	
2519	32887	c	2551	227	388	
2520	32888	В	2552	25	687	
2521	32889	В	2553	569	753	
2522	32890	lc	2554	147	384	
2523	32891	В	2555	210	419	
2524	32892	В	2556	1	1185	
2525	32893	lc	2557	93	257	
2526	32894	Ĉ	2558	41	375	
2527	32895	С	2559	155	579	
2528	32896	B	2560	1	375	
2529	32897	С	2561	37	351	
2530	32898	c	2562	39	518	
2531	32899	В	2563	310	493	
2532	32900	c	2564	83	373	
2533	32901	·B	2565	120	843	
2534	32902	С	2566	327	468	
2535	32903	В	2567	1	732	
2536	32904	С	2568	243	434	
2537	32905	C	2569	117	347	
2538	32906	С	2570	ī	363	
2539	32907	С	2571	1	219	
2540	32908	В	2572	82	390	
2541	32909	В	2573	1152	1737	
2542	32910	С	2574	294	524	
2543	32911	В	2575	1	345	
2544	32912	В	2576	106	1073	
2545	32913	В	2577	T	313	
2546	32914	c	2578	1	594	
2547	32915	c	2579	16	102	
2548	32916	c	2580	1	441	
2549	32917	В	2581	1	462	
2550	32918	В	2582	113	1257	

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
2551	32919	В	2583	l l	402	
2552	32920	В	2584	489	570	
2553	32921	В	2585	218	356	
2554	32922	С	2586	225	345	
2555	32922	C	2587	472	621	
2556	32923	В	2588	1	984	
2557	32925	В	2589	<u> </u>	1119	
2558	32926	В	2590	 	771	
2559	32927	В	2591	97	681	
2560	32928	В	2592	112	202	
2561	32929	c	2593	1	381	
2562	32930	c	2594	115	321	
2563	32931	c	2595	3	200	
2564	32932	В	2596	212	303	
2565	32933	c	2597	236	396	
2566	32934	В	2598	119	625	
2567	32935	C	2599	68	334	
2568	32936	c	2600	85	351	
2569	32937	В	2601	1	723	
2570	32938	c	2602	235	463	
2571	32939	В	2603	1	498	
2572	32940	c	2604	179	346	
2573	32941	В	2605	21	486	
2574	32942	В	2606	20	600	
2575	32943	В	2607	172	294	
2576	32944	В	2608	130	1200	
2577	32945	В	2609	61	243	,
2578	32946	В	2610	1	753	
2579	32947	В	2611	1	2274	
2580	32948	В	2612	1	1848	
2581	32949	В	2613	1	1263	
2582	32950	В	2614	412	654	
2583	32951	c	2615	176	658	
2584	32952	В	2616	310	628	
2585	32953	В	2617	1	579	
2586	32954	С	2618	145	309	
2587	32955	В	2619	298	353	
2588	32956	В	2620	163	594	
2589	32957	В	2621	1	468	
2590	32958	В	2622	1	552	
2591	32959	В	2623	1	876	
2592	32960	В	2624	140	1333	
2593	32961	С	2625	1	222	
2594	32962	В	2626	1	645	
2595	32963	С	2627	49	339	
2596	32964	В	2628	1	1944	
2597	32965	С	2629	79	189	
2598	32966	C	2630	513	767	
2599	32967	В	2631	114	230	
2600	32968	В	2632	24	629	
2601	32969	В	2633	98	230	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2602	32970	В	2634	99	462	
2603	32971	В	2635	127	1498	
2604	32972	В	2636	22	105	
2605	32973	В	2637	1	1173	
2606	32974	В	2638	403	660	
2607	32975	В	2639	58	507	
2608	32976	С	2640	103	480	
2609	32977	В	2641	1	657	
2610	32978	В	2642	1	508	
2611	32979	В	2643	1	999	
2612	32980	c	2644	ı	756	
2613	32981	С	2645	1	675	
2614	32982	В	2646	I	810	
2615	32983	В	2647	li .	334	
2616	32984	В	2648	1	781	
2617	32985	В	2649	76	211	
2618	32986	В	2650	1	687	
2619	32987	В	2651	1	753	
2620	32988	В	2652	37	1038	
2621	32989	В	2653	1	456	
2622	32990	В	2654	1	168	
2623	32991	В	2655	1	786	
2624	32992	c	2656	571	1278	
2625	32993	С	2657	96	548	
2626	32994	c	2658	391	504	
2627	32995	В	2659	1	183	
2628	32996	c	2660	i	381	
2629	32997	В	2661	1	642	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
2630	32998	В	2662	1	1164	
2631	32999	В	2663	i	471	
2632	33000	В	2664	1	972	
2633	33001	c	2665	75	182	
2634	33002	c	2666	125	226	
2635	33003	В	2667	1	462	·
2636	33004	В	2668	i -	422	
2637	33005	В	2669	81	616	
2638	33006	В	2670	197	713	
2639	33007	В	2671	i	882	
2640	33008	В	2672	i -	507	
2641	33009	c	2673	176	274	
2642	33010	В	2674	250	446	
2643	33010	B B	2675	19	118	
2644	33011	В	2676	21	120	
2645	33012	В	2677	373	389	
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2647	33014	В	2679	70	148	
2648	33015	C	2680	7	96	
		c	2681	-	550	
2649	33017	В	2682	360 55	1618	
	33018	ID.	2002	22	1019	
2650 2651	33019	В	2683	i	309	

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
2653	33021	IB	2685	1	11191	
2654	33022	В	2686	52	834	
2655	33023	В	2687	1	933	
2656	33024	c	2688	80	322	
2657	33025	В	2689	127	415	
2658	33026	В	2690	74	190	
2659	33027	В	2691	150	380	
2660	33028	В	2692	1	1098	
2661	33029	c	2693	185	502	
2662	33030	В	2694	1	180	
2663	33031	c	2695	257	498	
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2665	33033	c	2697	720	902	
2666	33034	č	2698	201	437	
2667	33035	č	2699	16	189	
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2670	33038	В	2703	777	1035	
2671	33039	В	2704	1	1200	
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2673	33041	В	2706	351	480	
2674	33042	В	2707	10	327	
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2676	33044	В	2709	36	189	
2677	33045	В	2710	54	3192	
2678	33046	В	2711	1	3423	
2679	33047	C	2712	5	280	
2680	33048	c	2713	1	88	
2681	33049	C	2714	1	153	
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2684	33052	B	2717	74	943	
2685	33053	c	2718	109	315	
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2688	33056	C	2721	1	486	
2689	33057	c	2722	87	441	
2690	33058	c	2723	85	276	
2691	33059	c	2724	86	280	
2692	33060	C	2725	108	254	
2693	33060	В	2726	1	930	
2694	33062	В	2727	23	847	
2695	33062	В	2728	19	182	
2695	33063	С	2729	190	300	
2696	33064	В	2729	67	650	
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2698	33066	В	2731	1	1149	
2699	33067	В	2732	1	263	
2700	33068	В	2733	73	676	
2701	33069	В	2734	1 .	414	
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SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
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2712	33080	c	2745	120	401	
2713	33081	В	2746	1	688	
2714	33082	В	2747	 	549	
2715	33082	В	2748	196	1647	
2716	33083	В	2749	1	378	
2717	33085	C	2750	2	166	
2718	33085	В	2751	1	807	
2719	33080	C	2752	343	532	
2720	33087	В	2753	1	885	
2721	33088		2754	32	247	
2722	33090	В	2755	1		
2723		В	2756	1	1152 885	
2724	33091	В	2757	87	359	
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2725 2726	33093 33094	В	2758 2759	117	418 1983	
		_		176	1045	
2727	33095	В	2760			
2728	33096	В	2761	25	187	
2729	33097	В	2762	1	315	
2730	33098	В	2763	1	351	
2731	33099	В	2764	1	396	
2732	33100	В	2765	12	350	
2733	33101	В	2766	1	411	
2734	33102	В	2767	1	1020	
2735	33103	В	2768	72	359	
2736	33104	В	2769	1	526	
2737	33105	В	2770	1	1233	
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2739	33107	В	2772	1	246	
2740	33108	В	2773	1	747	
2741	33109	В	2774	1	861	
2742	33110	С	2775	1	1278	
2743	33111	В	2776	1	630	- · · · · - · · · · · · · · · · · · · ·
2744	33112	С	2777	22	147	
2745	33113	В	2778	242	744	
2746	33114	В	2779	54	178	
2747	33115	В	2780	1	2277	
2748	33116	В	2781	1	204	
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2750	33118	В	2783	1	819	
2751	33119	В	2784	1	720	
2752	33120	В	2785	1	444	
2753	33121	В	2786	1	519	
2754	33122	В	2787	1	864	

No.	SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
Texas			1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
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2782 33150 B 2815 337 1512 2783 33151 B 2816 32 335 2784 33152 B 2817 I 1026 2785 33153 C 2818 I 1044 2786 33154 B 2819 I 1575 2787 33155 B 2820 I 1356 2788 33156 B 2821 I 3726 2789 33157 B 2822 158 627 2790 33189 B 2823 814 3116 2791 33159 B 2824 I 2667 2792 33160 B 2825 I 2778 2793 33161 B 2826 96 662 2794 33162 C 2827 163 245 2795 33163 B 2828 I 381 <							
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2788 33156 B 2821 I 3726 2789 33157 B 2822 158 627 2790 33158 B 2823 814 3116 2791 33159 B 2824 I 2667 2792 33160 B 2825 I 2778 2793 33161 B 2826 96 662 2794 33162 C 2827 163 245 2795 33163 B 2828 I 381 2796 33164 B 2829 47 378 2797 33165 B 2830 I 614 2798 33166 B 2831 277 528 2799 33167 B 2832 1 1059 2800 33169 C 2834 161 466 2801 33169 C 2834 161 466 <						1575	
2789 33157 B 2822 158 627 2790 33158 B 2823 814 316 2791 33159 B 2824 1 2667 2792 33160 B 2825 1 2778 2793 33161 B 2826 96 662 2794 33162 C 2827 163 245 2795 33163 B 2828 1 381 2796 33164 B 2829 47 378 2797 33165 B 2830 1 614 2798 33166 B 2831 277 528 2799 33167 B 2832 1 1059 2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 <	2787	33155	В	2820	1	1356	
2790 33158 B 2823 814 3116 2791 33159 B 2824 1 2667 2792 33160 B 2825 1 2778 2793 33161 B 2826 96 662 2794 33162 C 2827 163 245 2795 33163 B 2828 1 381 2796 33164 B 2829 47 378 2797 33165 B 2830 1 614 2798 33166 B 2831 277 528 2799 33167 B 2832 1 1059 2800 33169 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2804 33172 B 2837 1 111 </td <td>2788</td> <td>33156</td> <td>В</td> <td>2821</td> <td>1</td> <td>3726</td> <td></td>	2788	33156	В	2821	1	3726	
2791 33159 B 2824 1 2667 2792 33160 B 2825 1 2778 2793 33161 B 2826 96 662 2794 33162 C 2827 163 245 2795 33163 B 2828 1 381 2796 33164 B 2829 47 378 2797 33165 B 2830 1 614 2798 33166 B 2831 277 528 2799 33167 B 2832 1 1059 2801 33169 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2804 33172 B 2837 1 11929	2789	33157	В	2822	158	627	
2792 33160 B 2825 I 2778 2793 33161 B 2826 96 662 2794 33162 C 2827 163 245 2795 33163 B 2828 I 381 2796 33164 B 2829 47 378 2797 33165 B 2830 I 614 2798 33166 B 2831 277 528 2799 33167 B 2832 I 1059 2800 33169 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2804 33172 B 2837 I 11929	2790	33158	В	2823	814	3116	
2794 33161 B 2826 96 662 2794 33162 C 2827 1163 245 2795 33163 B 2828 1 381 2796 33164 B 2829 47 378 2797 33165 B 2830 1 614 2798 33166 B 2831 277 528 2799 33167 B 2832 1 1059 2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2791	33159	В	2824	1	2667	
2794 33162 C 2827 163 245 2795 33163 B 2828 1 381 2796 33164 B 2829 47 378 2797 33165 B 2830 1 614 2798 33166 B 2831 277 528 2799 33167 B 2832 1 1059 2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2804 33172 B 2837 1 1929	2792	33160	В	2825	1	2778	
2796 33163 B 2828 1 381 2796 33164 B 2829 47 378 2797 33165 B 2830 I 614 2798 33166 B 2831 277 528 2799 33167 B 2832 I 1059 2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2793	33161	В	2826	96	662	
2796 33164 B 2829 47 378 2797 33165 B 2830 1 614 2798 33166 B 2831 277 528 2799 33167 B 2832 1 1059 2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2794	33162	C	2827	163	245	
2797 33165 B 2830 I 614 2798 33166 B 2831 277 528 2799 33167 B 2832 I 1059 2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2795	33163	В	2828	1	381	
2797 33165 B 2830 I 614 2798 33166 B 2831 277 528 2799 33167 B 2832 I 1059 2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2796	33164	В	2829	47	378	
2799 33167 B 2832 1 1059 2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929			В	2830	1		
2800 33168 C 2833 354 491 2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2798	33166	В	2831	277	528	
2801 33169 C 2834 161 466 2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2799	33167	В	2832	1	1059	
2802 33170 B 2835 78 2700 2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2800	33168	С	2833	354	491	
2803 33171 C 2836 37 111 2804 33172 B 2837 1 1929	2801	33169	С	2834	161	466	
2804 33172 B 2837 1 1929	2802	33170	В	2835	78	2700	
	2803	33171	С	2836	37	111	
	2804	33172	В	2837	1	1929	
2805 33173 B 2838 36 612	2805	33173	В	2838	36	612	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nocleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
2806	33174	В	2839	189	498	
2807	33175	c	2840	302	430	
2808	33176	Ċ	2841	58	219	
2809	33177	c	2842	56	275	
2810	33178	c	2843	21	293	
2811	33179	c	2844	337	543	
2812	33180	В	2845	1	507	
2813	33181	c	2846	232	489	
2814	33182	c	2847	314	476	
2815	33183	c	2848	572	937	
2816	33184	Č	2849	259	528	
2817	33185	В	2850	1	597	
2818	33186	В	2851	li	564	
2819	33187	В	2852	368	732	
2820	33188	Ĉ	2853	58	375	
2821	33189	В	2854	608	1222	
2822	33190	c	2855	41	358	
2823	33191	c	2856	73	177	
2824	33192	В	2857	1	582	
2825	33193	c	2858	li	543	
2826	33194	В	2859	li	1538	
2827	33195	В	2860	40	704	
2828	33196	c	2861	303	407	
2829	33197	В	2862	131	336	
2830	33198	c	2863	64	156	
2831	33199	В	2864	180	712	
2832	33200	В	2865	1	1104	
2833	33200	В	2866	65	228	
2834	33202	В	2867	1	2172	
2835	33202	В	2868	i	1338	
2836	33204	c	2869	181	410	
2837	33205	В	2870	1	1137	
2838	33206	В	2871	69	1322	
2839	33207	c	2872	24	266	
2840	33208	В	2873	1033	1089	
2841	33209	В	2874	367	463	
2842	33210	В	2875	1	3256	
2843	33211	c	2876	278	466	
2844	33212	В	2877	323	4268	
2845	33213	В	2878	424	1711	
2846	33214	В	2879	567	643	
2847	33215	B	2880	1	258	
2848	33216	В	2881	i i	806	
2849	33217	В	2882	56	984	
2850	33217	В	2883	1	807	
2851	33219	В	2884	i -	396	
2852	33220	C	2885	107	411	
2853	33221	В	2886	1	678	
2854	33222	В	2887	1	246	
2854	33222	C	2888	41	316	
2856	33224	В	2889	1	300	

SEO ID	ICEO ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
2857	33225	C	2890	lı .	273	
2858	33226	В	2891	78	169	
2859	33227	В	2892	ı	882	
2860	33228	c	2893	1	246	
2861	33229	В	2894	i	639	
2862	33230	В	2895	1	411	
2863	33231	c	2896	427	522	
2864	33232	В	2897	158	826	
2865	33233	В	2898	275	310	
2866	33234	В	2899	429	933	
2867	33235	В	2900	1	560	
2868	33236	В	2901	i	798	
2869	33237	В	2902	45	384	
2870	33238	В	2903	845	983	
2871	33239	c	2904	171	422	
2872	33240	c	2905	139	360	
2873	33240	c	2906	188	436	
2874	33242	c	2907	76	303	
2875	33242	c	2908	362	574	
2876	33243	c	2909	42	347	
2877	33244	В	2910	1	766	
2878	33246 ·	В	2910	170	1381	
2879	33247	В	2912	274	543	
2880	33248	В	2912	768	2001	
2881	33248	В	2913	140	279	
2882	33249	В	2914	1	2858	
2883	33251	В	2916	1	321	
2884	33252	В	2917	1	552	
2885		В	2917	1	603	
	33253		2918	122	406	
2886	33254	С		508	679	
2887	33255	В	2920		942	
2888	33256	-	2921	1	753	
2889	33257	В	2922	1		
2890	33258	В	2923	136	326	
2891	33259	В	2924	445	625	
2892	33260	В	2925	1	639	
2893	33261	В	2926	1	1850	
2894	33262	В	2927	76	1341	
2895	33263	С	2928	184	495	
2896	33264	В	2929	1	226	
2897	33265	В	2930	1	972	
2898	33266	В	2931	57	1493	
2899	33267	С	2932	207	404	
2900	33268	В	2933	664	1647	
2901	33269	В	2934	1	1305	
2902	33270	В	2935	1	639	
2903	33271	В	2936	59	1108	
2904	33272	В	2937	276	1311	
2905	33273	В	2938	1	708	
2906	33274	В	2939	123	309	
2907	33275	В	2940	1	957	

SEQ ID	Iceo in No.	later	SEQ ID NO:	Nucleotide	Mustantida location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
2908	33276	С	2941	199	357	
2909	33277	В	2942	319	355	
2910	33278	В	2943	574	1044	
2911	33279	В	2944	1	426	
2912	33280	С	2945	1	381	
2913	33281	С	2946	145	301	
2914	33282	В	2947	1	1644	
2915	33283	В	2948	1	906	
2916	33284	В	2949	249	317	
2917	33285	В	2950	388	655	
2918	33286	С	2951	228	379	
2919	33287	С	2952	200	343	
2920	33288	В	2953	1	600	
2921	33289	В	2954	123	719	
2922	33290	В	2955	1	879	
2923	33291	В	2956	88	445	
2924	33292	В	2957	518	1508	
2925	33293	С	2958	1	414	
2926	33294	С	2959	202	408	
2927	33295	В	2960	1	351	
2928	33296	В	2961	1	378	
2929	33297	С	2962	84	194	
2930	33298	В	2963	1	306	
2931	33299	В	2964	238	354	
2932	33300	С	2965	326	331	
2933	33301	В	2966	1	1005	
2934	33302	С	2967	31	408	
2935	33303	В	2968	48	335	
2936	33304	В	2969	1	241	
2937	33305	В	2970	1	768	
2938	33306	В	2971	93	728	
2939	33307	В	2972	25	88	
2940	33308	В	2973	1	414	
2941	33309	В	2974	1	555	
2942	33310	В	2976	83	3457	
2943	33311	В	2977	59	1280	
2944	33312	В	2978	1	414	
2945	33313	В	2979	1	354	
2946	33314	В	2980	1	477	
2947	33315	В	2981	1	357	
2948	33316	В	2982	182	394	
2949	33317	В	2983	148	1104	
2950	33318	В	2984	494	641	
2951	33319	С	2985	44	310	
2952	33320	С	2986	303	395	
2953	33321	С	2987	229	407	
2954	33322	В	2988	195	707	
2955	33323	В	2989	713	1063	
2956	33324	В	2990	67	746	
2957	33325	В	2991	468	1010	
2958	33326	С	2992	1	258	
2957	33325	В	2991	468	1010	

SEQ ID	SEQ ID NO:	IN 1.4	SEQ ID NO:	Nuclcotide	IN and a section of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1.0.	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence	' '	
2959	33327	В	2993	1	282	
2960	33328	В	2994	139	767	
2961	33329	В	2995	1	133	
2962	33330	В	2996	136	291	
2963	33331	В	2997	172	634	
2964	33332	В	2998	1	435	
2965	33333	В	2999	503	1294	
2966	33334	В	3000	1	495	
2967	33335	В	3001	1	1416	
2968	33336	В	3002	1	321	
2969	33337	В	3003	1	378	
2970	33338	В	3004	1	337	
2971	33339	C	3005	I	474	
2972	33340	В	3006	1	633	
2973	33341	С	3007	142	423	
2974	33342	С	3008	226	360	
2975	33343	С	3009	45	281	
2976	33344	В	3010	1	369	
2977	33345	С	3011	2082	2558	
2978	33346	С	3012	99	356	
2979	33347	С	3013	312	467	
2980	33348	В	3014	89	463	
2981	33349	c	3015	16	357	
2982	33350	В	3016	239	541	
2983	33351	С	3017	176	345	
2984	33352	В	3018	1	2238	
2985	33353	c	3019	40	309	
2986	33354	В	3020	80	835	
2987	33355	В	3021	1	741	
2988	33356	В	3022	i	1005	· · · · · · · · · · · · · · · · · · ·
2989	33357	В	3023	185	3661	
2990	33358	В	3024	1	1539	
2991	33359	В	3025	1	1197	
2992	33360	c.	3026	258	584	
2993	33361	В	3027	103	905	
2994	33362	В	3028	1	159	
2995	33363	В	3029	72	642	
2996	33364	C	3030	195	424	
2997	33365	c	3031	350	454	
2998	33366	В	3032	1	1494	
2999	33367	C	3033	1	336	
3000	33368	c	3034	169	423	
3000	33369	c	3035	131	307	
3001	33370	c	3036	80	423	
3002		В	3036	1	663	
	33371			619		
3004	33372	С	3039		1068	
3005	33373	В	3040	1	441	
3006	33374	В	3041	124	453	
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3009	33377	C	3044	99	215	l

SEQ ID	ISEO ID NO.	Mar	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequeoce (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	1			sequence		
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3010	33378	В	3045	1	675	
3011	33379	В	3046	1	479	
3012	33380	С	3047	18	272	
3013	33381	С	3048	800	1097	
3014	33382	С	3049	I	231	
3015	33383	С	3050	1	777 .	
3016	33384	В	3051	194	328	
3017	33385	В	3052	1	633	
3018	33386	С	3053	431	838	
3019	33387	В	3054	1	450	
3020	33388	В	3055	684	1367	
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3022	33390	В	3057	28	420	
3023	33391	В	3058	28	280	
3024	33392	В	3059	1	1335	
3025	33393	В	3060	516	1396	
3026	33394	В	3061	1	1563	
3027	33395	В	3062	1	903	
3028	33396	В	3063	191	628	
3029	33397	В	3064	1	534	
3030	33398	В	3065	1	1134	
3031	33399	В	3066	ı	1248	
3032	33400	В	3067	1	1479	
3033	33401	В	3068	l .	1635	
3034	33402	В	3069	46	447	
3035	33403	С	3070	1	624	
3036	33404	c	3071	25	330	
3037	33405	С	3072	132	253	
3038	33406	В	3073	4	1011	
3039	33407	В	3074	392	814	
3040	33408	c	3075	414	557	
3041	33409	c	3076	74	328	
3042	33410	c	3077	1	678	
3043	33411	В	3078	1	5130	
3044	33412	В	3079	1	985	
3045	33413	В	3080	1	1671	
3046	33414	В	3081	146	556	
3047	33415	В	3082	1	732	
3048	33416	В	3083	136	753	
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3051	33419	В	3086	1	1221	
3052	33420	В	3087	58	1287	
3053	33421	В	3088	1	933	
3054	33422	B	3089	<u> -</u>	1317	
3055	33423	В	3090	1	771	
3056	33424	В	3090	1	2241	
3057	33425	В	3091	 	642	
3058	33425	В	3092	1	2664	
3059	33427	C	3093	1	513	
3060	33428	c	3094	52	174	
2000	J-3420	١~	2073	J-6	177	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
l				sequence	ì	
		<u> </u>				
3061	33429	C	3096	44	428	
3062	33430	C	3097	300	437	
3063	33431	С	3098	1	576	
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3065	33433	С	3100	1	801	
3066	33434	С	3101	298	480	
3067	33435	В	3102	503	720	
3068	33436	С	3103	1	756	
3069	33437	В	3104	1	355	
3070	33438	С	3105	1	1143	
3071	33439	В	3106	1	2256	
3072	33440	С	3107	537	966	
3073	33441	В	3108	1	2009	
3074	33442	В	3109	1	3021	
3075	33443	В	3110	1	1085	
3076	33444	В	3111	180	2069	
3077	33445	В	3112	1	375	
3078	33446	В	3113	31	127	
3079	33447	В	3114	47	452	
3080	33448	С	3115	149	440	
3081	33449	В	3116	119	538	
3082	33450	В	3117	1	900	
3083	33451	С	3118	1	270	
3084	33452	В	3119	1	344	
3085	33453	C	3120	72	245	
3086	33454	В	3121	1	822	·
3087	33455	С	3122	69	242	
3088	33456	В	3123	2129	2289	
3089	33457	С	3124	1	255	
3090	33458	В	3125	2129	2289	
3091	33459	В	3126	1	306	
3092	33460	С	3127	I	255	
3093	33461	В	3128	82	1254	
3094	33462	В	3129	1	468	
3095	33463	C	3130	2	250	
3096	33464	С	3131	166	357	
3097	33465	В	3132	423	3286	
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3099	33467	В	3134	1	4578	
3100	33468	В	3135	1	4322	
3101	33469	В	3136	46	325	
3102	33470	В	3137	58	289	
3103	33471	В	3138	1	1695	
3104	33472	В	3139	89	1195	
3105	33473	C	3140	317	541	
3106	33474	В	3141	314	992	
3107	33475	C	3142	95	222	
3108	33476	c	3143	26	172	
3109	33477	c	3144	40	255	
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3111	33479	В	3146	12	1358	
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SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
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3113	33481	C	3148	1	306	
3114	33482	C	3149	li .	771	
3115	33483	В	3150	149	360	
3116	33484	В	3151	ı	567	
3117	33485	В	3152	i	345	
3118	33486	В	3153	li	1233	
3119	33487	В	3154	144	773	
3120	33488	C	3155	1	417	
3121	33489	В	3156	85	525	
3122	33490	C	3157	251	679	
3123	33491	В	3158	1	1185	
3124	33492	c	3159	541	729	
3125	33493	В	3160	211	382	
3126	33494	c	3161	200	409	
3127	33495	C	3162	85	423	
3128	33496	c	3163	243	455	
3129	33497	В	3164	152	437	
3130	33498	В	3165	1	816	
3131	33499	В	3166	79	294	
3132	33500	c	3167	6	353	
3133	33501	c	3168	82	405 .	
3134	33502	В	3169	3	191	
3135	33502	C	3170	204	413	
3136	33504	В	3171	75	1449	
3137	33505	В	3172	173	738	
3138	33506	В	3173	1	324	
3139	33507	C	3174	299	1009	
3140	33508	В	3175	1	447	
3141	33509	С	3176	1	570	
3142	33510	В	3177	1	703	
3142	33511	В	3178	142	744	
3144	33512	В	3179	1	237	
3145	33513	C	3180	63	254	
3146	33514	В	3181	185	330	
3147	33515	В	3184	214	1333	
3148	33516	В	3185	61	423	
3149	33517	В	3186	19	2467	
3150	33518	В	3187	4	1085	
3151	33518	В	3188	157	341	
3152	33520	В	3189	222	656	
				249	999	
3153	33521	В	3190	416	2447-	
3154	33522	В	3191	187	1855	
3155	33523	_				
3156	33524	С	3193	38	166	
3157	33525	В	3194	1	1449	
3158	33526	В	3195	286	663	
3159	33527	В	3196	255	556	
3160	33528	В	3197	85	591	
3161	33529	В	3198	32	404	
3162	33530	В	3199	185	253	

SEQ ID	long in vo	13.1	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
NO.	sequence	liiou	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			· .	sequence		
3163	33531	В	3200	202	2862	
3164	33532	В	3201	448	833	
3165	33533	В	3202	1	1275	
3166	33534	В	3203	1	591	
3167	33535	С	3204	ı	291	
3168	33536	В	3205	1	744	
3169	33537	В	3206	338	523	
3170	33538	В	3207	1	435	
3171	33539	В	3208	1	477	
3172	33540	В	3209	1	2943	
3173	33541	В	3210	1	1719	
3174	33542	c	3211	113	280	
3175	33543	В	3212	1	1092	
3176	33544	В	3213	i	1470	
3177	33545	В	3214	i	426	
3178	33546	В	3215	i	747	
3179	33547	В	3216	321	2234	
3180	33548	В	3217	1	3057	
3181	33549	В	3218	i	537	
3182	33550	В	3219	1	2496	
3183	33551	В	3220	94	273	
3184	33552	В	3221	302	1432	
3185	33553	В	3222	35	1657	
3186	33554	В	3223	2	901	
3187	33555	В	3224	82	1479	
3188	33556	В	3225	224	411	
3189	33557	В	3226	328	429	
3190	33558	В	3227	27	1098	
3191	33559	В	3228	508	1765	
3192	33560	C	3229	1	321	
3192	33561	В	3230	251	415	
3193	33562	В	3231	695	1011	
3194	33563	В	3232	1	416	
			3232	45	1340	
3196	33564	В	3234	65	2087	
3197	33565	_			1149	
3198	33566	В	3235	1		
3199	33567	C B	3236 3237	1	108 384	
3200	33568	_		80		
3201	33569	В	3238		383	
3202	33570	В	3239	200	409	
3203	33571	В	3240	14	419	
3204	33572	В	3241	1	888	
3205	33573	С	3242	165	435	
3206	33574	В	3243	452	593	
3207	33575	В	3244	1472	4415	
3208	33576	В	3245	103	207	
3209	33577	В	3246	242	292	
3210	33578	В	3247	1	306	
3211	33579	В	3248	1	684	
3212	33580	В	3249	1	838	
3213	33581	В	3250	215	2593	

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GEO ID	Tero in vo.	151.4	SEQ ID NO:	Marata atlah	Thusbatide location of last	Amino acid sequence (X=Unknown,
SEQ ID NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3214	33582	C	3251	80	376	
3215	33583	В	3252	I	639	
3216	33584	С	3253	52	288	
3217	33585	В	3254	I	1197	
3218	33586	В	3255	39	2809	
3219	33587	В	3256	1	609	
3220	33588	С	3257	269	418	
3221	33589	В	3258	1	561	
3222	33590	В	3259	347	922	
3223	33591	В	3260	52	339	
3224	33592	В	3261	235	434	
3225	33593	В	3262	74	2676	
3226	33594	В	3263	90	675	
3227	33595	В	3264	1	1440	
3228	33596	В	3265	288	752	
3229	33597	В	3266	1	804	
3230	33598	С	3267	109	451	
3231	33599	В	3268	1	1122	
3232	33600	В	3269	1	768	
3233	33601	В	3270	380	2743	
3234	33602	В	3271	1	1296	
3235	33603	В	3272	322	591	
3236	33604	В	3273	174	464	
3237	33605	В	3274	1	384	
3238	33606	С	3275	320	385	
3239	33607	В	3276	53	485	
3240	33608	c	3277	175	205	
3241	33609	В	3278	216	316	
3242	33610	В	3279	1	921	
3243	33611	В	3280	22	453	
3244	33612	В	3281	168	817	
3245	33613	В	3282	1	477	
3246	33614	В	3283	190	1062	
3247	33615	В	3284	116	787	
3248	33616	В	3285	130	697	
3249	33617	В	3286	1	901	
3250	33618	В	3287	i	342	
3251	33619	В	3288	1	677	
3252	33620	В	3289	i — — —	624	
3253	33621	В	3290	li	756	
3254	33622	В	3291	<u> </u>	624	
3255	33623	В	3292	130	429	
3256	33624	В	3292	95	516	
3257	33625	В	3294	120	524	
3258	33626	В	3294	51	425	
3258	33627	В	3296	647	1015	
3260	33627	С	3296	518	841	
3261	33629	c	3297	67	294	
3262	33630	В	3299	1	1212	
3262	33631	С	3300	187	453	
		В		188	492	
3264	33632	l _B	3301	1100	474	

SEO ID	ISFO ID VO-	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
l				sequence		
3265	33633	В	3302	123	647	
3266	33634	C	3303	1	219	
3267	33635	В	3304	1	690	
3268	33636	В	3305	<u> </u>	930	
3269	33637	В	3306	552	722	
3270	33638	В	3307	84	304	-
3271	33639	В	3308	328	1104	
3272	33640	c	3309	300	593	
3273	33641	C	3310	1	87	
3274	33642	В	3311	i	819	
3275	33643	c	3312	122	334	
3276	33644	В	3313	1	318	
3277	33645	В	3314	764	977	
3278	33646	c	3315	379	471	
3279	33647	В	3316	1	1194	
3280	33648	В	3317	i	1800	
3281	33649	C	3318	273	506	
3282	33650	В	3319	1	1689	
3283	33651	c	3320	48	212	
3284	33652	c	3321	1	507	
3285	33653	c	3322	117	251	
3286	33654	В	3323	89	845	
3287	33655	c	3324	ī	651	
3288	33656	C	3325	48	212	
3289	33657	С	3326	I	864	
3290	33658	В	3327	223	839	
3291	33659	С	3328	1	189	
3292	33660	В	3329	36	144	
3293	33661	В	3330	56	389	
3294	33662	В	3331	1	597	
3295	33663	В	3332	1	606	
3296	33664	С	3333	1	426	
3297	33665	В	3334	1	696	
3298	33666	В	3335	1	417	
3299	33667	С	3336	1	594	
3300	33668	В	3337	1	228	
3301	33669	С	3338	1	879	
3302	33670	В	3339	1	405	
3303	33671	C	3340	33	152	
3304	33672	В	3341	224	429	
3305	33673	В	3342	578	4588	
3306	33674	В	3343	1	288	
3307	33675	В	3344	77	1479	
3308	33676	В	3345	132	875	
3309	33677	С	3346	120	395	
3310	33678	В	3347	1	729	
3311	33679	C	3348	8	133	
3312	33680	С	3349	171	359	
3313	33681	В	3350	I .	1098	
3314	33682	В	3351	1	1547	
3315	33683	В	3352	1	933	

SEQ 1D			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for pentide	coden for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or peptioe sequence	ucicion, (-possible nucleorate insertion)
3316	33684	В	3353	I	1989	
3317	33685	В	3354	1	595	
3318	33686	С	3355	62	559	
3319	33687	В	3356	1	153 .	
3320	33688	В	3357	1	768	
3321	33689	В	3358	1	969	
3322	33690	В	3359	217	358	
3323	33691	С	3360	449	961	
3324	33692	В	3361	1	1799	
3325	33693	В	3362	80	1327	
3326	33694	В	3363	111	258	
3327	33695	В	3364	112	429	
3328	33696	В	3365	147	390	
3329	33697	В	3366	I	585	
3330	33698	В	3367	1	2290	
3331	33699	В	3368	19	4071	
3332	33700	С	3369	1	183	
3333	33701	С	3370	1	183	
3334	33702	С	3371	44	283	
3335	33703	В	3372	1	954	
3336	33704	В	3373	1	384	
3337	33705	В	3374	709	773	
3338	33706	В	3375	1	3294	
3339	33707	В	3376	83	1229	
3340	33708	В	3377	1	1512	
3341	33709	С	3378	30	200	
3342	33710	A	3379	3	322	
3343	33711	A	3380	530	1489	YAGNESHPPSLPRYLRRSRHCG CRPPPLEVETPTQACNAPQRRR TYSTSLACLGRAGI-WLPSVSSP YLVLSSCQEQPHHCCPPSTPRPS WSPLPGMFSA/SSPGQVPAQCD LSQEDSSDSPAEQVLPPSSGSH NTLYLGCKRFSAFILNCEPPSKL LKARPQVSELSWNPDFVA/S/SA ARPRGPGCSTGQSASKTPPPPS HPHTGHSL-WSEEK-KDSDSRPN QSAFPGCSVDLQFSHKLRPYLI HP/SESLGTVGNRPSQEGHELPP AFFSRMGPEQHLPVVVLPFTGA FAVVLPCPFLVSSSAWHFKVKH PSIPLLRGEK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Aminn acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3344	33712	A	3381	296	1255	YAGNESHIPSLPRYLRRSRHGG CRPPPLPVPTPTQACNAPQRRR TTSTSLACLGRAGLWLPSVSSP YLVLSSCQEQPHHCCPPSTPRPS WSPLPGMPSASSPGQVPAQGD LSQEDSSDSPAEQVLPPSSGSH NTLYLRCKERSAFILNCEPPSKL LKARPQVSELSWNPDFVAS/SA ARPRODPCSTGRQSASKTPPPPS PHPTGHSL WSEEK*KDSDSRPN QSAFPGCSVDLOFSHKLRPYLI HPSESLGTVORNPSOGGHEV APFSKMGPEQHLPVVVLPFTGA FAVVLPCPFLVSSSAWHFKVKH PSIPLLRGEK
3345	33713	A	3382	81	702	RAAFSPPAPVSSIPAS PAHSSPPASTSS PPAPLSSAPAHTSSLPAPVSSPPA STSSPLVAGSGGSTTRSLPPGL GALLTHSVAPYPGGQPPPAAAD DP*TMAPAGWGSHNPRGCSCSP VAAGAGPPFASFGPLR*AGSQ TFQILQVEVFLVVRHFSPSTP/PS VMLYPPPFSTPPTLRAPRPPIPPS P
3346	33714	A	3383	3	231	PMLLEVSVADRDAV*TFWQAPI GESQQGALGFWSKALQSSADN NS/PFQITMQPELPIMNWVLSVP SSHKMGHAQQH
3347	33715	A	3384	3	355	KIPGTSTSVKFLGVQ*CGTCQDI PSKVKDKLLHLAPPTIKKEAQR LVGLFGFWSQHIPHLGELLRPIY RVTRKAASFEWGPEHEKALQQ VQAALQAALPLGPYDPADQPL CNLNCLS

SEO ID	SEO ID NO:	Mat	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, :=possible nucleotide insertion)
				sequence		
3348	33716	A	3385	2	1076	LCORLLLAEPNEKPGSLGNVM
						AVARIEIGICEYYHEKTTEKALI
	1	ĺ				SHGVLAGSTIKGVRSFQRNLEL
	1					KLPATERATANAIELLTVLDQA
						YENFAPQILPSTGSPTSQETAOF
		1				KANONKPLVRGKGSPHEAIRYI
						SAAHREWKPAILTSAIRSFCST
	ŀ	1				WLVFTSKNFPKLVTQHGSTIAG
1		1		1		NGQSSDETQVQGAAWKSDSRC
l				Į.		TKRQIPTWILAEGNNAGAQLDI
		1		1		PGPTIPAPNCSLKVPQSWSTTPS
						MPSSLGKAYWLLACYWALVET
		l				E/RLAMGHQVTM\KPELPVMN
						WVLSDPSSHKVGGAQQHSINK
		l				WKWYIRNRARAGPEGTTLPLT
						KALTLWLKKYSNVLMLVEFTG
						LTMFPDILKQLE
3349	33717	Α	3386	1	1416	MAQYPILDFLKVGQLLGNCAL
						GKGNDQTFRGLLDTGSELTLIP
						GDPKHHCDPPVKCAAIDLANA
İ				1		FFSIPVHKAHQKQFAFGWQGQ
ŀ						QYTFTVLHQGCMNSLALCHNL
						QRELDCFLTPEDITLDHYIDDIM
						LIGSSEKEVANTLDLLFWDYRH
	ľ					EPLRLANYSPFERQLLACYWAL
		1				VETECLMMGHQVTMRPELPIM
	l					NWVLADPSRHKVGNAQQHWK
		1				CAVHT/IIKWKWYIRDWAQAG
	1	l				LEGTS*LYWPRASRYQQGHQD
	ŀ					LFILRSDLPSQVFIRDKLMERRN
						RRTGRTEKARIWEVTDRTVRT
	ì	ŀ				WIGEAVAAAAADGVTFSVPVT
į.						PHTFRHSYAMHMLYAGIPLKV
		ŀ				LQSLMGHKSISSTEVYTKVFAL
	22512	_	2207	50	(02	DVAARHRVQFAMPESDAVAM
3350	33718	B A	3387	153	693 578	A DIO/CEDNOCVEVEVA DI TUT
3351	33/19	A	3388	133	310	ARIQ/GSRNQGVEVEVAPLTVT PSDPLANVLLPVPATLPSAGLEI
		ł				LVPEEGRLPPGDTTMMPLNWN
	l	ŀ				
						LRLPHGHFGLLLPLNQQAKKG
	1	ŀ				VAVLGGVIALDCQDEISLLLYK
		ŀ				GDLTVMVEDKEEQNHILHGSR
3352	33720	A	3389	3	402	QREREPSKTGSPL GRHAVGDIEAEDGGGVRGPHP
3332	33/20	^	3389	ľ	402	GGVYGLQQSHPGGGDPVWED
		1		1	1	GHPGLPGAOORGO*ROOACAH
						,,,,,,,
		ŀ				HKSPSGAG*G*LPGP/AQS/AGN PDPKSPGPAPCLVGSSRNETPG
		l		1		AMGAPSRNGSPPTAGLGVGDG
l		1		1	1	TGSPSEAV
3353	33721	Α	3390	141	320	TOSTSEAV
دردر	127/21	M	13390	1141	320	

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	sequence	of peptide sequence	deletion, -possible increating insertion)
3354	33722	A	3391	T	1464	HLKGLGNDTPRVCSCLIG*T*L(
						DCH*LO\EASPTSVEVREPRTSV
						NKD/SPKSLLYSCSYSYFDEPVE
				l		LRSSSFSSWDDSSDSYYETHLL
						HLKLV*PNLAVFNCRPTARRKF
						DYEPVENTDEAQKTFCKTAHN
						LWSLTFPFPCLL*YETRARLER
3355	33723	Α	3392	3	1189	
3356	33724	Α	3393	1	867	PGRPT/LSEWI/QNTLGVNVEHK
						TTSKASLNPRDTPPSVVNEDFL
						HDLKETNISYSQEADDRVFRAH
	Ì					GHCLHEIFLLTEGMFERIPDIVL
						WPTCHDDVVKIVNLACKYNLC
						IIPIGGGTSVSYGLMCPADETRT
1				ŀ		IISLDTSQMNRILWVDENNLTA
						HV*AGITGKELERQLKESG\YC1
į .				1	1	G\HEPRFPWSSSTVGGWVSTRA
						SGMKKNIYGNIEDLEIVHFSDN
				ł		DLSCIELDRLIEIVLPSSGIPLLD
ŀ						GYSTEIHMPVHLETSTTMCIVTI
						IHSSMKLETLRMSMSINCRKDK
3357	33725	A	3394	1	890	MSKSESPKEPEQLRKLFIGGLSF
1					i	ETTDESLRSHFEQWGTLTDCVV
						MRDPNTKRSRGFGFVTYATVE
					1	EVDAAMNARPHKVDGRVVEP
						KRAVSREDSQRPDYFEQYGKIE
	1	l				VIEIMTDRGSGKKRGFAFVTFD
						DHDSVDKTVIQKYHTVNGHNC
						EVRKALSKQEMASASSSQRGRS
	1			•		GSGNFGGGRGGGFGGNDNFGR
						GGNFSGRGGFGGSHGGGGYGG
						SGDGYNGFGNDGSNFGGGGSY
						NDFGNYNNQSSNFGPMKGGNF
						GGRSSGPYGGGGQYFAKPRNQ/
		ļ				GGYGGSSSSSSYGSGRRF
3358	33726	Α	3395	2	441	DGMEKVDTAMNARPHKVDGR
1						FVEPKTA VSREDSQRPGAHLTV
	1					IKM/FKE/DTEEHKLRDYIEQYG
						GGNFSGCAGFGGRSGGGR*GG
						SGNGYNRFDNDGSNFGGGGSY
1				1		NDFGNYNDRSSNFGPIKGGNFG
		ļ	2206	<u> </u>	1	GRSSGPYGGGSQYFAKP*NQ
3359	33727	A	3396	3	404	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3360	33728	A	3397	2	762	MNARPHKVDGRVVEPKRAVSR
-						EDSQRPGAHLTVKKIFVGGIKE
						DTEEHHLRDYFEQYGKIEVIEI
						MT\DRGSGRKRGFVFVTF\DDP\
						DSVDKIVIQKYHTVNGHNCEV
						RKALSKQEEMASASS\SQRGRS
						GSG\NFGGGRGGGF\GGNDNFG
						RGGNFSGRGGFGGSRGGGGYG
						GSGDGYNGFGNDGSNFGGGGS
		ĺ				YNDFGNYNNQSSNFGPMKGGN
						F\GGRSSGPYG\GGGQYF\AKPR\
		İ		İ		NQGGYGGSSSSSSY\GSGRRF
3361	33729	A	3398	I	3737	
3362	33730	Α	3399	5	633	DLREWSWARRTAWEPRGKRV
						RGK*AFKEIQCP*QQKE/SMSGL
			1			LLLKVVAKEMTWLPPLSAIQAP
1						GKVEPTKFPFPNKLMFSWWYIE
					1	TTTASAKVIGYKPSVLNCATLR
						VQIMSHYHSYRHLASLLVEGSA
						TLPGHSHILGPLIRHPDKVSAGK
				1		PRVLGLQLLKEDCSSQPAAKPQ
		1				GPHRLCSSLILHRARARLGPEQ
						RETKVPFSKGTTH
3363	33731	Α	3400	2	816	QVPTMVDWAGWSPGLWTTCS
		1				GTGGGGAEQGWANWSLVLPG
		i				VLAGTSLETFSPLS*GLTFSSLLL
		1				MQISAASLNFSSENGIFFSTTLP
						GCKFSKFLCSASLLKWNAFSST
		l				QVTS*MLCCSEISSTRYPKSSL*
		1			r	SSKFHKSLEQGQNAASLFAKT*
1		l				QESPLLQLPTSSSSPSETTSAWIS
						LSISLSVFLSKLFDKSLESSKLS\
						TFSSVLLSPPNCSNLCLLPSFKV
1		1				ACTFLGTFLRSTSLHWYQFTVL
				l		VCFHPADKDILKSEKKKRCKEK
3364	33732	Α	3401	1	485	LFKAVLHDPHLKLLSLYGTSLS
		1		I		HTDVSHLCETLKHTTCKIEELM
		l				LGTCDISDEGCEDIASVLACNS
	1	l				KLIHLSLVENPEKDKRM\CCCA
1	1	1				LETLMLMYCCLICVSCEDISHV
		1			1	LFCSKSLSLLDLGSNFLEDNEV\
l		1				HLLCEALKH*DACKTWRSLNF
						DWVGYLGC
3365	33733	С	3402	952	1164	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide lucation of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3366	33734	A	3403	13	163	IAVSKODPITSLEQEKEPWNMK
						ICEMVDESPAMCSSFTRDL.WPF.
	ł					ODIKOSFOOVILRRHGKCEHEN
		1			İ	LOLRKGSASVDEYKVHKEGYN
İ						ELNOCLTTTOSKIFPCDKYVKV
1		1				FHKFLNANRHKTRHTGKKPFK
	l	1				CKKCGKSFCMLLHLSQHKRIHI
		1		,		RENSYQCEECGKAFKWFSTLTR
		1				HKRIHTGEKPFKCEECGKAFKQ
1		l				SSTLTTHKIIHTGEKPYRCEECG
		1				KAFNRSSHLTTHKIIHTGEKPYK
1	l					CEECGKAFNQSSTLSTHKFIHA
		1				GEKPYKCEECDKAFNRFSYLTK
		1				HKIIHAGEKP\YNCEECGKGFN
		1				WSSTLTKHKRIHTGEKPYKCEV
	İ	l			1	CGKAFNESSNLTTHKMIHTGEK
						PYKCEECGKAFNRSPQLTAHKII
						HTGEKPYKCEECGKAFSQSSIL
		1			1	TTHKRIHTGEKPYKCEECGKAF
	l					NRSSNLTKHKIIHTGEKSYKCEE
						CGKAFNQSSTLTKHRKIHTRQK
	1					PYNCEECDNTFNQSSNL/N*/HK
				1		IIHTGEKLYKCQECGKASKQSF
3367	33735	A	3404	3	345	TLTKH*ILFNK
3368	33736	В	3405	282	694	
3369	33737	A	3406	586	1403	VSETALADGRCWFRKCOSHLC
	1					LASTTGKC*TSTLQSGRDYTEN
	İ					GESAQEGETGLPERRLAHCT*L
	İ					AEVHRRQPD*TQENRP/SKMGI
		ı				MTSS/AAKDHLDNKCQRQDSIP
		1				GSSRGPSPLTMGAQDTLPVAAA
						FTETVNAYFKGADPSNTPSVLV
						EQLLSKRRSNPIMDHGGHKVPC
	l					SLPPLLTHPNRRQRELKMYGSH
		1				KAVAQPSPLQDRLQQCAVPTP
		1				VTGWTNSRAALGDIFSTWGSLL
		1				LRTSTPKKAAARARPMCPCPGA
		ļ				YNTSYPLAPYFWR
3370	33738	A	3407	1	421	FRHSMNGCEKDSSSTDSANEKP
		1				ALIPREKKISILEEPSKALRGVT
		1		1		GPNIEKSVKDLQRCTVSLTRYR
	1	1		1		VMIKEEVDSSVKKIKAAFAELH
						TCIIDKEVSLMAEMDKVKEEA
		1		1		MEILTARQ\RKAEALKRLTDL\A
3371	33739	A	3408	l I	403	S\QMAEMQL MEILTARQKKAEELKRLTDLAS
33/1	33/39	l ^A	3408	l'	403	QMAEMQLAELRAEIK/*WFSEN
		1		1		ELGNSDLCSYSCYCLAAOKLSC
	1	1		I		OCYLGGTAHSAPGIAKRKTSOL
	1	1		1		I*PLP
				L	L	1 1 1 1

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X≡Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3372	33740	A	3409		756	
3373	33741	A	3410	2	1849	ORRRRNTPGWSGFQGLTRAPA
				Ī		LFPRLIFQSSSETRLLSGTLLWIP
		l				RAYSTRSKMAELNTHVNVKEK
		l				IYAVRSVVPNKSNNEIVLVLOO
						FDFNVDKAVQAFVDGSAIQVL
		l	,			KEWNMTGKKKNNKRKRSKSK
						QHQGNKDAKDKVERPEAGPLQ
		l				POPPOIONGPMNGCEKDSSSTD
						SANEKPALIPREKKISILEEPSKA
		l				LRGVTEGNRLLQQKLSLDGNP
		l			1	KPIHGTTERSDGLOWSAEOPCN
1		ĺ				PSKPKAKTSPVKSNTPAAHLEI
		1				KPDELAKKRGPNIEKSVKDLQR
1	ŀ	1				CTVSLTRYRVMIKEEVDSSVKK
		1				IKAAFAELHNCIIDKEVSLMAE
		1				MDKVKEEAMEILTARQKKAEE
		1				LKRLTNLASQMAEMQ\LAELR\
						AEIKHFVSERKYDEELGK\AAR
						FSCDIEQLK AQIMLCGEITHPK\
						NNYSSRTPLQAPCWPLLNA\HA
						ANLWGKQSNF\SRKSSTHNKPS
					ŀ	EGKAATPKMVSSLPSTADPSLR
		l				AMPANKQNGSSNQRRRFNPQY
		ļ			l	HNNR\LNGPAKSQGSGNEAEPL
		l				GKGNSRHEHRRQPHNGFRPKN
						KGGAKNQEASLGMKTPEAPAH
		1			1	SEKPRRRQHAADTSEARPFRGS
		l				VGRVSQCNLCPTRIEVSTDAAV
		L_				LSVPAVTLVA
3374	33742	Α	3411	1	489	MAEVQVPVLHGRGHLLGRLAA
		l				IVAKQVMLGWKVVVVRCEGIN
		1				ISGNFYRNKLNCSFRTPSCIFRW
						TVRGMLPHKTKRGQAVLDHLQ
		1				VFDGISPLYDK/K/KRMVVPAAL
		1				KVVRLKPTRKFAYLGRLAHEV
		1				GWKYQAVTATLEKRKEKA*IH
		_				YRKKKQLMRLRKQA
3375	33743	A	3412	2	260	A STANDARD AND A STANDARD A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD AND A STANDARD A STANDARD A STANDARD AND A STANDARD A STANDARD AND A STAND
3376	33744	Α	3413	I	612	AEVQVLVLDGRGHFLCRLADI
		1				VAKQVLLG\RKVVVVRCEGINI
		1			l	SGNFYRNKLKYLAFLRKRMNT
		l	1			NPSRGP\YHFRAPSRIFWRTVRG
		1				MLPHKTKRGQAALDRLKVFDG
						IPPPYDKKKRMVVPAALKVVR
						LKPTRKFAYLGRLAHEVGWKY
						QAVTATLEEKRKEKAKIHYRK
				1		KKQLMRLRKQAEKNVEKKIDK
	L		L		L	YTEVLKTHGLLV

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleatide	Nucleotide location of last	Amino acid sequence (X=1/nknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3377	33745	A	3414	734	1488	MTKDPWLKQSGSSDTSPAASP
3377	33743	n	3414	/ 37	1700	GHFRAVPRAPRARGTVVHHRH/
		1				LCLSSWPSSS/RVPPGCASYTPA
		1			•	STAAGALPYQAQRRQGVLRRY
						TTYLRV*HFLPRGLPEGFORGP
		l				RVPPPPPCPMAAEPELGHALKL
		1				LD\LREIVSFLYYFFFFFLRRSLT
		1			1	LSPGWRDLGSLQ\PLPHGFKAIF
1	l	1				/SCFSLLSGWD\YRHTATHAQLI
1						FVFLVEMGF/TPMFARMASIS*P
					İ	CDPPDSASQDAGITGVSHQVW
1		l				RERLFLDEGGGGCP
3378	33746	A	3415	48	966	WSOVVTIVTVVVTVSGSNHGN
3378	33740	l^	3413	40	300	HTQASHEGYRHPMRAQVSH/G
1						ECR/PSHEGHRHPMRTQASHEG
		ŀ				HRRPMRTQASHEGHRHPMRTQ
						ASHEGHRHPMRGTGVP*EHRH
İ						PMRAQASH/GEHRR/HH/GEHSC
		1				PMRAQASHEGTGVP*EHRC/HH
		ŀ				ENTGVP*GHRCPMRMQASHAG
ŀ						HRHPMRVQASHEGHRCPMRTQ
		1			•	VSHEGHRRPMRVQASHENTGV
						P*GAOASHEGTGVP*EHSHPMR
1		1				AQASHENTDVP*GVQASHEGY
		1				RRPMRTQASHEGHRCPMRAQT
						SHENTGVP*AAQYRP*EAGAPO
1		l				GGOGWOETGADRST
3379	33747	$\frac{1}{\lambda}$	3416	8	432	NSKLPPVVTSQQMRFMY/DPQT
						DOHMKINFPEOLPLDEFLOKTOP
		ı		1		KDPANYILHAVLVHSGDNHGG
		l				HYVVYLNPKGDGKWCKFDDD
		l		l		VVSRCTKEEAIEHNYGGHDDD
		l				LSVRHCTNAYMLVYIRESKLSE
		l			i	VLOAVTDHDIPOOL
3380	33748	A	3417	38	2865	SFRWDSKKHTGYVGLKNOGAT
		1				CYMNSLLOTLFFTNOLRKKLL
		l				MGALPWEGALAPWV*ALDTDP
İ		1				SLPCSTCLTTARTCTSL\QQCHA
		l				DQCRWQTRWQGSSRW*WQQE
		l				EIGQEREEGVEYAKRVLLGPPY
		1				SISDCTHMESSLPPCSS*DPGSF
				1		OFHEERAEDEKSEGRGPSCSCT
						QPPPW*SLGEGLGECR*ESSSSY
		l		1	1	CSLAGLSLIIP*ETRGERLOEAS
				1		QGQPESPFGEV*HPALVSLDLA
				l	l	E*OGRAEKHGCTETH

SEQ ID SEQ ID NO: Met SEQ ID NO: Nucleotide N	PGAAVAD PPPPRLAA AQAAAD EQQLSEPE LTQNPVIN DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
	PGAAVAD PPPPRLAA AQAAAD EQQLSEPE ITQNPVIN DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
3381 33749 A 3418 2 3515 YVRVSLPPPPPAAGRI DAREEEEAAPPPPP ARPGOOPRIPAAGE MNHQQQQQQKAGI DMEMEAGOTDDPPR GNVALSDGHNTAEEI WRSEATFGFTVSES PPCEVRNLPWKIMVN PHQKSVGFELQCNAE CHAQAVLKIINYDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	PPPPRLAA AQAAAD EQQLSEPE ITQNPVIN DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
DAREEEEAAPPPPPF ARPROSOPRPPAAGE MNNIQQQQQQGG MNNIQQQQQQGG DMEMEAGDTDDPPR GVVALSDGHNTAEEI WRSATFQFTVERFS PPCFVRNLPWKIMVN PHQKSVGFFLQCNAE CHAQAVLKINYRDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	PPPPRLAA AQAAAD EQQLSEPE ITQNPVIN DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
DAREEEEAAPPPPPF ARPROSOPRPPAAGE MNNIQQQQQQGG MNNIQQQQQQGG DMEMEAGDTDDPPR GVVALSDGHNTAEEI WRSATFQFTVERFS PPCFVRNLPWKIMVN PHQKSVGFFLQCNAE CHAQAVLKINYRDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	PPPPRLAA AQAAAD EQQLSEPE ITQNPVIN DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
ARPGSOPRPPAAGE MNNQQQQQKAGI DMEMEAGDTDDPPR GNVALSDGHNTAEI WRSEATFOFTVERFS PPCTVRNLPWKIMVM PPIQKSVGFFLQCNAE CHAQAVLKINTYDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	AQAAAD EQQLSEPE ITQNPVIN DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
MNHQQQQQQKAGI DMEMEAGDTDDPRR GNVALSDGHNTAEII WRSEATFQFTVERES PPCFVRNLPWKINW PHQKSVGFFLQCNAE CHAQAVLKINYDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV	EQQLSEPE ITQNPVIN DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
DMEMEAGDTDDPPR GNVALSDGHNTAEII WRSEATFQFTVERFS PPCFVRNLPWKIMVN PHQKSVGFFLQCNAE CHAQAVLKINYRDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	ITQNPVIN DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
GNVALSDGHNTAEEI WRSEATFQFTVERFS PPCCVRNLPWKIMVM PHQKSVGFFLQCNAE CHAQAVLKINTYDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	DMEDDTS RLSESVLS MPRFYPDR ESDSTSWS DEKSFSRRI
WRSEATFQFTVERFS PPCEVRNLPWKIMWN PHOKSVGFELQCNAE CHAQAVLKIINYRDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	RLSESVLS MPRFYPDR SDSTSWS DEKSFSRRI
PPCFVRNLPWKIMVM PHQKSVGFFLQCNAE CHAQAVLKINYRDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	MPRFYPDR ESDSTSWS DEKSFSRRI
PHQKSVGFFLQCNAE CHAQAVLKIINYRDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV	SDSTSWS EKSFSRRI
CHAQAVLKIINYRDD SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	EKSFSRRI
SHLFFHKENDWGFSN VTDPEKGFIDDDKV 3382 33750 B 3419 36 335	
3382 33750 B 3419 36 335 VTDPEKGFIDDDKV	IFMAWSE.
3382 33750 B 3419 36 335	
2292 22751 A 2420 2 1602 CDIVTTACCOCCODU	
WQICSLPKHLIPPEAP	
RRKPVWVKSMMLG*	
DPPTTAKCRTCSPQEI	ETGPAGT
QGQAARQLERRKLPF	PYVQT/PP
RPDQLKGVCSLQTDA	AISLAPTA
ERHSRLLPPPSRQQPT	SAGTEA
GACPNTRRPSGLQLP.	AAV\QTPS
GQTPSVPKPGLEPTSL	.PVGSG/PI
SASHSQ/PVSKINKK*	*VCESPY
METFP*DAKRTRHKR	ADTARR
GEPLRPRTSVPRRTVF	PAPSEKLR
GSRRGEPTPAAPRRD	PRRAGSL
THAGPPGG*RHR*PG	WPRGTA/
AKTPVAAEALIAAAA	PLALHRI
PLGAPPQLPAAPAP/R	LALALRG
ASAA/RPRVAPSAASF	PQRCLLR\
GPPSPQPSPAPGPVAP	SAQGRG
AVPGGVLAVLLPGAF	PRLSGKRP
AAPRGGDTPAQGQVI	PLAARAP
REGPGHGREPVIEELE	ERRGAEL
RSGKGGTRSEGVRGC	GRARGIV
YGGAHGPEVGKDKM	IPLKPRNL
SAPVAIGGLLHGAGII	RFLNLAL
HSPAVDFGQIT	
3384 33752 A 3421 3 498 IIDPTQYRPMVPNKVS	SSPC*WLP
TITQVHPDNEAEPIPS	/PARSCAP
ICGVP/AYGSPLSQSS	VS*TRQ*F
PSCSQSL**GSPTLVN	
NSGSRGG/VSFDEDTS	SQHCYPG
TG*GQQPLQ*SRNHA	GPPGG*M
T*VTGVAERDK/PPKT	PVGRRG
THSQPPRRSP	
3385 33753 A 3422 I 270	

SEO ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ļ		sequence		
		<u> </u>			1220	l
3386	33754	Α	3423	Įī.	1899	MGFCHIGQAGLKLLTSKDLPAS
						AFQSAGIAGFWLLDGISGPILGQ
						REACCPAGNSNKELKQENSAL
			l			AEQLQVVLIDKAGMQCDLEEL.
ļ						KKKLELTELTLQQLSSWCEAPD
				ł		ANQQLQQPTDERAQLEAHLGQ
ŀ	l					VMEWLKYLQMEREQYAEYLH
			l	l		GESAMWWQRMREMSEQIGHLI
ł				l		VPGICEMGGAQPEVVMGLGFV
				l		EVHTLREERVHSMSRVQELETI
						LAELRNQVAEPLPPEPPAGPSE
					Ì	VEQKLQAEAEHLWKELENLAG
						QLQAQVEENEGLSHLNQEQE\G
						LLRLLEQEEKLLEQEERLLEQE
		i		1		ERLLEQEERLLELQESLLEQKR
						KAASFLS*TPTPGAPSRALRGK
						YVTSYQSQRSV/REDVDRENEY
					ì	ISRLAQDKEEMKVKLLELVLQL
			1		İ	VGDCNKWHGRFLAAAQNPAD
						EPAPWDPAPQEIGAANKQGGLF
		1				PGCCLVTPGGFHGDCRGAYGA
						QSSPDSQQAQNPDLAVAGKAA
				l		FWEFKEHQESLTLLKSWGRRK
1					1	SGSGQAAQLREGSRCAAARRH
						LARALPAARMPKRKVISTEGAA
						KEEPKRTSASLSAKPPAKVEAO
1						PKKAAAKDKSSDKKTQTKGKR
1		1				GAKGKQAEVANQETKEDLPAE
		1				NELSSLYSFYARSLILAFIIHLRM
3387	33755	IA	3424	198	364	FLII*YEGINCSRIVNLTRTAWCF
		1				FSG*IFRQKKCKQKGKGEQREN
		ł				RPEVANPRN
3388	33756	A	3425	3	238	GVCPPRGRSCSDFKADSLYSFP
1	1	[1	1		CPSRCGS*ESSTOTCSGFWTGCT
1 .		1	1	1		ALHRWRGMPERCPPESRDS*TR
1						FPOSSLPGHKT
3389	33757	A	3426	3	681	HIRGPRYSGHHSAFGCPYSDMN
15505	55757	Γ.		ľ		LKKEATLHDRLREQTQAN\LES
		1				DSSHSKSKSLCSLNFNGKHEKV
1		į.				NSOPRLYOOAKCLKIKGKEDID
i						LDNLFREYSVEQAQQVLHQSV
				l		SMSTVSAHPFRDLPLGREQHCK
1		1	1			LLPGVADIRASQVARWTVDEV
1		1	1	1		AEFVOSLLGCEEHAKCFKKEOI
1						DGKAFLLLTQTDIVKVMKIKLG
		1		l		
						PALKIYNSILMFRHSQELPEEDI
	L	<u>L</u> .	L	L		ASGQEVRG

SEO ID	ISEO ID NO:	Met	SEO ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon far peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3390	33758	A	3427	30	981	TODPWPSLPVLWSRASSDPAAC
3390	33738	l^	3427	150	261	HRAEHI*TYWPWKLEGT\DIWI.
				l		VLYMPLVQPDNFIKKHSHLPTY
	ì			1		CLFKEDVKFPFRTCRLTYCWLN
	ľ					YTEEITYLHTKKVSVGOSAVRE
	l					EFAAACTWSIRIGEKLAILLSLY
						LCROOALLNMRMSVPIHESGV
1	į .			}		AQRSPVMDKLAQYSVEQAQQV
1						LHQSVSMSTVSAHPFRDLPLGR
					ĺ	
			1			EQHCKLLPGVADIRARQVARW
1						TVDENLHGLIQTKQTPHLDESIS
1		1				KGESPALVVTELRMCMTATEP
		1				LVPTKNPYQERGHIGDSFLHYT
		l				DQEPQPWDQSSVHPTPAPIYSV
	20750	ļ.	2.100		0.51	SSGFRVTRGSDI
3391	33759	A	3428	1	864	MVSALPEVGRAQILRLIAYIRSP
		1		İ		APPVVGVERAARRPAQAFGLV
				ľ		ALPSTDATVFANQPLARACIGA
		1		•		ARHREPDAPGQSAWVGEECLK
	1	1	ľ		1	DALRSPETPKLGSLSPPCQDTRF
						GRASNDFSLEMGYSSLSAARLK
		l			1	IHGQVFQCCGPGPLRTL\HWTQ
						S*TYLNILALET*GAQNQP*EW
		1				QAVD*GAPGLFSHTLGVFPR/RL
		1				PQHPKQIICFQNYEYSVEQAQQ
		l				VLHQSVSMSTVSAHPFRDLPLG
						REQHCKLLPGVADIRASQVAR
		ŀ				WTVDEPYSSAPRGPELSAGANS SRGA
3392	33760	A	3429	201	336	QQTPGKAVHAPFIADQSLT*EL
100/2			,		l	VSVFPQFQLFPYRR*DSHSGKS
3393	33761	A	3430	600	768	TDTSSYHGSG*PAR/NG*MHSFI
100.0						RCLLLK*GIEPCALNGDSVLKS
						RTDVTFTPVNITTKVKSVEMHN
	į .					EALSRALPGDNVGFKNVSKMF
	į .					VMATLLFSDCIHNTFDQMWRT
						KEHNEARWSLOSSGDKVMKEN
	1	1		1		DELRDSVSQLQKQTLSLKSPKI
	1		1			ALGESLISCRERAEIEIVDKQTQ
		1		l		ALIMGVADLQGRVNAQLHQVS
			1	l		TVKVRDWKRMGPYNLECGTV
						GRTLIKLWTLSL
3394	33762	ΙΛ.	3431	1655	1841	EHQAEAEGGDGGPRSLPMKPG
1			1			SPLMPDKAQRKQVRSRHGRGG
	1			1		RGGG*AGPGIPGKPGSPVSP
3395	33763	A	3432	1	1773	
E272	1-2,02	1.,	55	Ŀ		L

of peptide sequence		SEQ ID NO: in USSN	Nucleotide		Amino acid sequence (X=Unknown,
			location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
			sequence		
33764	Α	3433	648	1884	LDPEVAWAKWQHSTVKGPQK
					QFAFSWQGQQYTFTGLPQGYIN
					SLSLCYNLIPRDPD/RL/SLLQNI
	l				TLVHYIDDIMLIGSSEQELAYTL
					DLLVRRLCAKGWEINLTEIQEA
					STSVKFLRVQWCGACQDIPSK
			ŀ		MKDKLLHLFPPTTKKKASLFGF
		i			RRQCIPHLECGPEQEKALQQAQ
					AAVQAAVPLERYDPADPMVL/
					V/ELTWLWPLLSAQFASSGDQH
			i		*ALHMAPFLGVVSQLPGGKLIII
			1		DIFHHGKGRVLFSLE*TLTPDM
					GLPILHIMLLPRLPSVNSQNALS
	ŀ				TVMPGFTGPGIKGWKWHHSPS
					PLVIH*QNFCFLFP*HYVLLA*R
					S*FQRKEPCHQET*Q*FH*TGS*
					GCQLDTLGSCYF*VNKLRRELQ
		1			CWLG*LTQTIKMKSVYYSITEN
	l				CWMKRSPVKRRKILELEEA
33765	Α	3434	1	2223	
33766	Α	3435	1	1078	MNKEMSGQTFVGKQNSVRMP
					KIISGLGVQKPNRQWRLVQDLF
					IINEAVVPLYQAVRNPYTLLSQI
					PEETGWFTVLDLKDALFCIAVH
					PDSQFLLAFEDPLNPTSQLTWT
					VLPQGFRDSPHLFGQALAQDLS
					QFSYLDTLVLRYVDDLLLAAPS
					ETLCHQATQVLLNFLATCGYK
			l		VSKLKAQICSQQVKYLGLKLSK
					GTRALSEERIOPILAYPHPKTRK
			l		QLRGLLGITGFCQIWIPRYSEIA
			l		RPLHTLIKKTOKANTHLVRWTE
			l		EAEAAFOVLKKALTOAPVLSLE
			l		TGODF\SLYVTEKTGIALGVLTO
					HYGEERNS*LPTEYLSNIRKPLG
			l		DYYWLYRNLKRWOSYTARVIR
			l		KERKGK
33767	A	3436	1	1677	
		33765 A	33765 A 3434	33765 A 3434 I	33765 A 3434 I 2223

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
3400	33768	A	3437	1	2052	WYLVVVAVVVVLVVAVIVV WVVVVAAVVVVLVAVIVV VVVVAAVVVQAVVVVVVV VVVVVAAVVVQEDNOHKTGA INNNTTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHIMTIK QVSLTPPKITLAHQQWIQTKKK VLIYLKKHSQVNKIPRNPTYVEG CEGPFQGELQTTAQQNKGGHK QTEDHISMLMDRKNQYCENGH TAQAVPNPTYLLSQIPEDAEWF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGFR NSPHLFQQALAQDLSQFSYLDT LVLRYMDDLLLATHSETLCHQ ATOALLNFLATCGYKVSRA QLCSQQVKYLGLKLSKGTRTLS EERIQPILGYPHPKTIK,QLTAFL GTIGFCQIWPRYSKIARPLNTRI KETQKANTHLVRWTPGAEVAF QALKKALTHAPVLSLPVGQNFS LYVTEKYTGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRYNIY ANSIGREREFLTSKGTTLVSHQ AIKGLLLAVQKPKEVAVLHCW GHQKGKEREIEENRQALIEARR AARQDPPLEMLTEGPLAFELA
						MATARAELSLAIHHCCLPPPPQ TRCWLPSLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPRS EKTRLATILEAACCHFGSGPPPS WELWEOGPPVTVOTHILRSHL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3401	33769	Α	3438	294	2340	EKCRHNCSSRVWOSLVSOSVW
						ATEGOYGRTKNARPVQVK\DS
		1		1		ASFPYORRYPLRLEAOOGLOKI
		1				VKDLKAQGLVKPFNSPCNTPIL
						GVQKPNGQWKLVQDLRIINEAI
				l		VPLYPAVPNPYTLLSOIPEEAE
						WFTVLDLKDAFFCIPVHRESOF
		1				LFAFEDPSNPTSQLTWTVLPQG
						FRNSPHLFGQALAQDLSQFSYL
						NTLVLRYLDDLLLAAHLETLCH
						QATQKKTGIALGVLTQVQGTSF
	ļ.			ŀ		OPVAHLSKEIDVVAKGWPHCL
		1				WVVAAVAVLVSEAVKIIOGRE
		l				LTVWTSHDVSGTLTAKGDLWL
		1		}		SDNLLLNQALLFKRPVLRLHTC
				l		ATLNPATFLPNNKEKIEHNHOO
		l				VIVQTYTIQGDLLEVPLTDPDL
						NLYTNGSSFVEKGLRKAGIHPS
						ROWTPLWPKAGPEMLSKROVL
						ESGILKAFLVPYLLVAVLGSIDF
						NGKPPVAVFSLSQAHRFLCAT
					1	WLLLGYGEVWIHSHTAIKTYO
			İ			RRRSQDGRIGTAPVYSSQRERR
						RRRVISAFPSEGIPTDLOLRVLS
ŀ		ŀ				VRRKTNKQKGHPHQKPICTSPS
				ļ.		SRPKVDKTTKMGKKONRKTGN
			İ	l		SKTOSASPPPKERSSSPATEOSW
i				1		MENDFDELREEGFRRSNYSELR
1						EDIQTKGKEVENFEKNLEECITR
				l		ITNTEKCLKELMELKTKARELR
						EECRSLRSQCDQLEERVSAMED
3402	33770	A	3439	2	350	YKVSKPKAQLCSQQVKYLWLK
		Γ.	1	1		LSKGTRALSEERIQPILAYPHPK
		1				TLKQLRGILGITGFCRIWIP\R*S
		l				SPTGQE/FSLYVTEETGIALGILT
						QVQGTSLQPMEYLNKEIDELDQ
	1	1	1			GRTH
3403	33771	A	3440	1	897	
3404	33772	A	3441	1	429	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3405	33773	A	3442	3	957	NKIPRNPTYEGCEGPTOCELQT TAQONKGGIKQTEDHSNLMD RKNQYCENGHTAQAVPPYTL LSQIPEDAEWFTVLDPKHAVFC IUVTVLPQGFRNSPHLFGQALAQ DLSQFSYLDTLVLFWADDLL ATHSETLCHQATQALINFLATC GYKVSKPKAQLCSQVKYLGI KLSKGTRTLSEERIQPILGYPH KTLKQLTAFLGITGFCQIWIPRY SKIARPLNTRIKETQKANTHLV RWTPEAEVAFQALKALTHAP VLSLEVGQNTSLYVTEKYTGIAL GVLTGELISWON
3406	33774	A	3443	146	1303	GVLIGEVISWO ATEGGYGRIKNARPYOVKUS ASFPYORRYPIRLEAQGLQKI VKDLKAQGLVKPFNSPCNTPIL GVQKPNGQWKLVQDLRIINAAI VPLYPAVPNYTLLSQIPEEAE WFTVLDLKDAFFCIPVHRESGF LFAFEDPSNFTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSVL LFAFEDPSNFTSQLTWTVLPQG FRNSPHLFGQALAQDLSQFSVL UTVLYRYDDULLAAHLETHLCH QATQKKTGIALGVLTQVQCTSF QPVAHLSKEIDVVAKGWPHCL UTVWANAVAVLVSEAVKIIQGRE LTYWTSHDVSGTLTAKGDLWL SDNLLLNQALFKRPVLRUHTC ATLNPATFLPNNKEKIEHNIQQ VIVQTYTIGGDLLEVPLTDPDL NLYTMGSSFVEKGLRXA

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertinn)
3407	33775	A	3444	1	1647	MNKEDYNDDDDDNGDIKYLPDI
		l			\	KTGYNKTVQIPITSENSTVGLSN
l		l				TEADEMORLKCERDDALKEVN
		l	İ]	TLKRRTKGGKHLTLKVTYTLSE
		l	i			TNLHKNYLWECILMGQLGCYE
		1		l		ILRKPSPALGLTPEHKGNVGHT
						GEKTGAG/PATSRPPDSFPN**G
					į	PPFNPNGTKGDRQRGKQQTKE
		l		ŀ		CQYSPIMPTPSSGRRRIWSSQ\R
						HVPFSLSDLIDLAVPNPYTLLSQ
						IPEEAEWFTVLDLKDVFFCIPVH
ŀ						PDSQFLFAFEDPLNPMSQLTCT
						VLPQGFRDSPHLFGQALAQDLS
		1				QLSYLDTLVLQYVDDLLLAAC
		i				SETLCHQATQALLNFLATCGYK
						VSKEKAQLCSQQVKYLGLKLS
	1					KGTKALSEECIQPILAYPHLKTL
						KQLREFLGITGFCRIW/NFQALL
						LERPVLQLCTCATLNPVTFLPD
						NE\EEYNCQQIISQTYATRGDLL
						EVPLTDPDLNLYTDGSSFVEKG
						PQKAGERRAVLASQTSLTPLGR
						NGRSIPATLALESKELVKSVRA
						LLDMDCAIPFLVGTSIVDPYLK
						YEPTTKNHLIMVQGEKNCITGR
3408	33776	A	3445	1	2217	
3409	33777	Α	3446	1	749	MNQSDQEMTGAFVHMKSYTG
						LISGVAVKMERHIYQDRRIAIEK
	1					EFNSCRTGCMGDWSFTITQIRL
		į				LENTGIRVFKDNLVEEAEWFTV
						LDLMDAFFCIPVHPDSQFLFAFE
						DPSNPASQLTWTVLPQRFKNSP
					i	HLFGQALAQDLSQFSYLDTLVL
	1	1				RYMDDLLLAAYSETLCHQATE
		ĺ				ALLNFLATCGYKVSKPKAQLCS
		ĺ				QQVKYLGLKLSKGTRDLTTFLP
		1	1			VNEEKIE/P*LSTSNCSKLRCSRG
		L				TSRGSLG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3410	33778	Α	3447	I	1374	MPLLQMIATPLQQSLISTEDEM
		l				DELTEVGFERWVITNFTEEPSPA
		l				LGFTPEHKGNVGHAGKGPLESS
						SPDPFLCGQEKQEKGAGLLHRC
						YPLRLEAKQGLKKIVKDLKAO
						GLVTPCSSPCNTPTLAVOKPNG
						QWRLVQDLRIINEAVVPLYPAV
					l	PNPYILLSQIPEEAEWFTVLDLK
		l			ŀ	DAFFCIPVHPDSQFLFAFEDPSN
					İ	PMSQLTWTVLPQGFRDSLHLFG
					i	QALAQDLSQFSYLDTLVLQYM
					ľ	DDLLLVTHSETLCHQATQVLLN
				1		FLATCGYKVSKLKAQICSQOVK
		1		1		YLGLKLSKGTRALSEERIOPILA
		l		i		YPHPKTRKQLRGLLGITGFCQI
				l		WIPRYSEIARPLHTLIKKTOKAN
						THLVRWTPEAEAAFOVLKKAL
						TOAPVLSLPTGODF\SLYVTEKT
						GIALGVLTOHYGEERNS*LPTE
						YLSNIRKPLGDYYWLYRNLKR
		l				WQSYTARVIRKERKGK
3411	33779	В	3448	I	2862	
3412	33780	В	3449	94	1248	
3413	33781	A	3450	I	3805	MQWEEAEKDPSGSCVFQRPPV
		1		i		ALVFPLHSKWTLVNSPPSSGDP
						YVPGRPAQSGQLSLSPAPPYVL
						PGPGKIKQAGNNPSLTSIYRSEV
						FCAHRHLHPPQLVCARGHIGSA
				l	1	HLSVDRGSLIWEVLESTVWART
1						NEWSPVTRTVLISALASTHIPQP
				ł		CESRPPVPPEYEVTVLRSQGTA
						QLPPWSSSTSWRLTDPSCPKHA
						AWLTDLASSKGPAAGGTGSFS
						QPGTLTSTRTNPLKKEKSPEDL
						KQIKIDLGKFSDN
3414	33782	A.	3451	Į.	444	YSLVEFHTLVLQKSDVEAVF/S
						KYCFIVGCSVHKGFAFV*YVNE
i i	ŀ		ĺ			RNARAAVGGD\DSSSFDLDHDF
l				1		QRDYYDRMYSYPAHVPPPPIAR
						AVVPSKCQHVSGN\RRGKSGFN
1			İ			SKRGQRGSSKSGKLKGDDLQAI
						KKELTQIKQKVDSLLENL
3415	33783	Α	3452	3	93	
3416	33784	Α	3453	117	316	SSATFSAL*ETLPSNTMASSSFD
1		l	l			LDYDFQRDYYDRMYSYPARVP
						PPPPIARAVVPSKRQRVSGNTS

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*-Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
i				scquence		
3417	Toogos	_	3454	1102	Linco	ETLPSNTMASNVTNKTDPRSM
3417	33785	A	3434	102	1059	
						NSRVFIGNLNTLVVKKSDVEAI
	l l					FSKYGKIVGCSVHKGFAFVQY
	ŀ			l		AYE\RNARAAVAG\EDGRMIAG
	ľ					Q\VLDINLAAEPK\VNRGKAGV
	ŀ					KRSA\AEMYGSVTEHPSPSPLLS
	l l					SSFDL\D\YDFQRDYYDRMYSY
						PARVPPPPPIA\RAVVPSKRQRV
				Ì		SGNTSRRGK\SGFNSKSGQRGSS
	I	ŀ		1		KSGK\LKGDDLQ\AIK\KELTPD
ł	į.					KTKKWDSLL\ENLEKI\EKEQSK
	1					QAVEMKNDKSEEEQSSSSR/VK
	l .					KDETNVKMESEGGADDSA\EE
	i i		1			GDLLG*MNDNE\DRGDDQLE\LI
						KDDEKEAEEGEDDRDSANGGG
3418	33786	Α	3455	299	509	
3419	33787	В	3456	16	101	
3420	33788	Α	3457	1209	1828	GNCDSPARPARPPHRQGCPRPS
				1		PPPRGRPRALGPTRASAARAPA
						DLPPPAAPHPAPAALVPHTAAP
						KA\RNALPGSPGALTEGAVLLP
	i					NAGARPRRPRSSEKP\GPAPSWP
	1					RIPGFRTGAPPPATPVLAAGGL
ļ						APPSPGLAGQQVALPSQVPADT
	i					QSGVKSGSQDRGRN*QSAGSA
	1					GGGARTQVPGPLRMWKRAVW
						PGDWAPHPANI
3421	33789	Α	3458	387	772	PHRKQAEPPRHHERLGRRVRH
	1				ĺ	HARHGRGSRPDTAAEAAGGCG
						DPRAFOOLERRLRHPPLRWOGL
						LRRORLLREEPRRSLL/QTS*S*C
			ĺ	1		SPVTRPSSGCSSPRSWMETRRG
	1					APAPPAPRSRNKPTTWWPH
3422	33790	A	3459	362	608	FFFFFLNRVLLCHPG/WS*SGNH
	1	1	I	I		QWQSWLNS*PQTPGLK*SSFLC
	1			1		FRKWWDYKHEPLYPAKPHFEF
						LFGSSLOVREFFGKIKV
3423	33791	В	3460	1	612	E. SEEDQ FREIT GRAIN
3723	122121	ь_	13400	Ľ	1012	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3424	33792	Α	3461	1277	2152	SRAAPTCFSWLPCGASTCPWL
		l				MWAMSGRMVAPLQRVLRAAP
		l	1			GLEGTLGGROHPGTPPSVLHFS
ł		l				LTMNSMFGLQDFNVTPLAAQA
l	İ	l	ľ			TLPPGSPGRPTLVPSTAAPNSLO
		ł				MFTGGHGA*FPRWQPQPPSGVS
						/SHGAPPGVPHYCROGRSPGKRV
						QRKWLESEVQAQGP*EPDPTOL
						OTSTRTACG*GPPSQADPDPDP
		ļ				TRPRTPDLDPNCMRLRTPKPGR
		1				ROSRPH\GPRTPTQTDPDPPVOP
		1				PAPEVKPORPP/WAARAPSDTA
		1	1			AS*GGLTCNSRPIREGOMGSPSP
		1				AGSLLLGAL
3425	33793	Α	3462	1	2064	MDGQCSHYCVKTDLRVHSPFT
		1				TGAVHADOSCCKTTSARWEDT
		i				CDLTGSKKTLVISNIVIRTRSDD
		l				KLENEWETQSQNRNRVKPTAA
		l				DPCRNE/NEHSS*EKHPEVLQES
		l				ANDRURDNERVSQRQSQPTTVS
		l				QRQSQPTTESEPTTES/RQRQSQ
						RQRQSQPMTESETMTELQKMT
						ESANDRVSQRQSQSQRQSQ\QR
		l				QSQRQRQSQSQ*QSQSQRQSQS
						QRQSQ\QRQSQSQRQSQ\QRQS
						QRQRQSQRQ*QSQSQ*QSQPTT
						ESEPTTEVSQRQNQRQRQSQP/
						DDRIRDNDRVSQRQNQRQRQS
				1		Q\Q*QSQRRQSQSQRQSQPTTES
						EPTTESANDRVSQRQSQSQRQS
						Q\QRQSQSQ*QSQPTTESANDR
						VSQRQSQSQGQSQSQRQSQS/D
				l		DRVSQRQIQSQHQEDRPPKYQN
				i		KNVQVHA/DDKPRSDPQRRRNL
				ŀ		TPPVKTAERRPHQEHVVKGEK
						ATSPSRHSTSTAPTRPPSAETAH
						VNVMCGGDMAHINQGHVEAP
						QGSHEKHVGAARDQYERRDA
	l	l		1		QSEKSQQVQTTGLRVHVSRRPP
		l				HDGSLTSTGLRVHVSRRPPHDG
	l	l				SLTSTGLRVHVSRRPPHNGTVT
	ŀ	l		1		STGLRVHVSRRPPHDGSLTSTG
	l					LRVHVPRRPPHDGSLTSTGLRV
						HVPRRPPTTALSHPLDVSICRTL
		l				NAYPEMLTGERSTFPCVNVKN
						EKAVESKKDTPFKCESKESWI
3426	33794	Α	3463	1	424	

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence (X=tinknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide scquence	of peptide sequence	deletion, \=possible nucleutide insertion)
3427	33795	A	3464	1	492	MDESSFRGSITQSGSAKTAGLT
						GFCKLCKTSSWHTGAAQILEGG
					l	MEKANSPQYADPQTHLSWHTL
				İ	1	PPGSQATSANESNVNFLSLPDT
						NSPÉIRPDHSPPVPDRSVSPLEHI
			ŀ			PRTFPKPGTG/PPHINTVTNPSA
						GAPR*E*PS*SGFNPGCFQLVRP
						SRISGTPV
3428	33796	A	3465	107	543	KREGWKEESDFWDGSHLPPLN
	İ					SRCSTRKGRKTGRCGAATAAA
		1	l		1	SSPREGRRPPPSWAGHPCLGSC
						QWLRSCR/RGLAMAPGALPAL
						GEEEGPGASGLSAEL/RASERGL
						GQGLGPAALHS*ASPTPWAPVR
						PEPPRRAPPPAPWRPVPL
3429	33797	Α	3466	27	1021	STQTWPVSEETGSPPQRNRC*SS
1		İ			l	HQPDTASWVLQREYSHRKGTA
			1		1	PRGMQGTLPLCPSLSGCRSPSCP
		1				AAARPPRPRAVRFPPPATAAAS
				İ	ŀ	SPREGRRPPPSW/RRPSLPRGLP
		l	•			VASELPEGLAMAPGVLPALFGS
				ŀ	ŀ	TLPL*AVT/PH*ECL/PASLLKPA
						RP*THREK*TTPDVQP*EL*HSP
						*RSAASLQEGPQLHS*SQ*DQEP
						TNSGHTYTLGTGR*FYTVCQFL
						WLG*TYRSSHRPGFACRCLEPG
						SAAPCPSHCLSAGPEGTL*AAC
						LGKVPGRSAPRSDQWSPGGRA
						PRGVPPPPLSRGHCKALASCAP
						SADA\REPPHRALLGSPKVHTP
3430	33798	A	3467	807	1428	GSDRLQPQPLLFGRDVLLLLPS
						GPAIPASGLASVFGAAGRAGHG
		ı				SGGSA*TWGRGRTRRERPLGG
		1				AGASE\PGSVGPRGA\GWVSGP
		l				VRAPPRAAPGTLAPSSGRCRAP
		ĺ				PPRRAQACVALTCPGPGGRCPL
						PMDRPALAMP/SHL/HPRPGQV
		1				APRWSPCSRRREEKGRHERVDI
			ĺ			GHSHLVFALTLFLP*FGGGGKT
						EA AQNS WRIPPAG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3431	33799	Α	3468	68	1153	LLKMFRAKAACLTSMAWVLPP
		ĺ				LSLIVLVILSPGSFILQITFTLLEP
						VLRRPSSAEKPLEPGPSSSPSSG
				ł		RARGA\RPALPAAPKPLASPEA
			ŀ			GMAVPGWGRR\SPSRREEAGA
			İ			VACLSLTVFSGKWICQQAP/SA
	ĺ		l			WGCCC*D*GKLVHRST*RCAR*
l						KYPGLKPDQEGYCQPGAPVEV
	Ì		1			HPRCRDFPS/VLRRNLGFSALAQ
				ŀ		SEYLW*DHS/CVLVVG/PVLFC*
1				ŀ		TLFASFPIRLYPEELLA/HKVTQ
1					•	CPSLVSPCNWLSAGGGRKFEPA
						LRRPSSAERPLAPYPSSSPGAGR
				l		APQPWPALPAAPKPLASPEAG
			l			MAGPGGRRTTSLPKRRGCGCS
			l			RPASSCFSSLSGWAARVERRQM
						ASIPEIALLFPSPL
3432	33800	Α	3469	1	248	FRPAPIPSSAPRGPTEPVLRRPSS
						AEKPLEPGPSSSPSSGRARGAM
İ						ASPSSSSEATGKPRGRDGSPRM
	ľ					G/VGGRPSRKEEAGAVAGGGK
						RTARGLRGRGGPAATGQEGDR
				l		HPYRWRRQRSGILHEF*AASGF
				l		PPPPNHGRHTVQAEPPEPWPAL
1						PAAPKPLASPEAGMAGPGGRR
						TTSLPKRRGCGSCCRGEAHSPT
						TARTGEDAPRPGREETGTQTGG
						DRRGAA/RGSP/RSPWA/CIRAPL
				ļ		PSLGVAPG/VPSGRLAHGDILISP
						CTLPHSELGSPGH*TQANFL*DP
						GRRRTVLWKVFQGRSRKG*EG RGPGRGHNYDGSVTPGNFIA*S
		ļ				
						PS/PLPLPPSFTWTLPKTRIPECS
						GVTKCSGTLGTRVW/RPGSWG LHPGSAPP*LRRPSSAEKPLEPG
						PSSSPSSGRARGAMASPSSSSEA
						TGKPRGRDGSPRMGEEDVPPE
2422	22001	_	2470	266	500	TGKPKGKDGSPKWGEEDVPPE
3433	3380I 33802	C	3470 3471	365	589 465	MVTTTCYCKKAKPIPRRCSAKE
3434	33802	A	24/1	ľ	403	WSCQLPCGQKLLCGQHKCENP
1	1		1	l		CHAGSCOPCPRVSROKCVCGK
1			1	l		KVAERSCASPLWHCDOIKE/CR
1			1	l		SOSCS*RRKTKTTG\ELEAFENR
1			1	1		LKGRRKKNRKRDEVAVELSLW
1				l		OKHKYYLISVCGVVVVVFAWY
			1			ITHDVN
L			L		l	ITIDAN

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3435	33803	A	3472		444	YSLVEFHTLVLQKSDVEAVF/S KYCFIVGCSVHKGFAFV*YVDK KYCFIVGCSVHKGFAFV*YVD RNARAAVGGMYSSSFDLDHDF QRDYYDRMYSYPAHVPPPPIAR AVVPSKCQHVSGNYRRGKSGFN SKRGQRGSSKSGKLKGDDLQAI KKELTQIKQKVDSLLENL
3436	33804	c	3473	190	265	
3437	33805	A	3474	144	316	
3438	33806	A	3475	3	342	
3439	33807	В	3476	180	1370	
3440	33808	A	3477	102	1054	ETLPSNTMASNYTNKTDPRSM NSRVFIGNLTNLTVKKSDVEAI FSKYGKIVGCSVHKGFAFVQY VNERNARGAVAGEDGRMIAVG QVLDINPGLQSPKVNRGKARC ETDLQAEMYGLLF*PWTYDFQ RDYYDRMYSYPARVPPPPPIAIR AVVPSKRQRVSGNTSRRGKSGF NSKSGQRGSSKSGKLKGDDLQ/ AIKRELTQIKQKVDSLLENLEK IEKEQSKQAVEMKK**SQKLEQ SQLR*KKDTET*C*RLEVLKGG AD\DSA*GRGDLL\DDDDN*RS GGIDQLEVLIKDDEKEAEEVGD DRGQRPMGGDDSLST
3441	33809	С	3478	216	350	
3442	33810	А	3479		3048	MGLMVLNVENCSSFGWIGRAP PRNTTVDLNSGNIDVPPNMTSW ASFHNGVAAGLKIAPASQIDSA WIVYNKPKHAELANEYAGFLV ALGLNGYLTKLATFNIHDYLTK GHEMTSIGLLLGVSAAKLGTM DMSITRLLSIRPALLPTSTELD VPHNVQVAAVVGJIGLVYQGIT AHRHTAEGPVGLR*DGLLFLKC NTALTOSHTP*AAGLALGMVC LGEQGPCCGVWEELGERETFK DLIFNRKAPEGSNAT
3443	33811	A	3480	173	422	AAAERGAEEASGGAPPGILEDA GRERRGSGGGR*AGPVGDSKD GVGAV*PPQPHSHRDHHQ*PGP
		_	L			LGGPGCSG*PHLREGLET
3444	33812	С	3481	241	426	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
			l	sequence		
3445	33813	Α	3482	3	826	RGEEAVSGKAGPDSPRAVLRG
		l				QGQVWGAAAERGAEEASGGG
		Ì		[TQGEGGREVFDS*GTCSLGFPS*
		l				PGEQLMGLVYTLGG*PHSHRD
		ĺ	1	ľ		HHQ*PGPLGG/HGCSG*PHLRW
		1				VPVSALGGRGVGADQLVRVAQ
		1				GSPETPCSLSGESWPA/GLPGPT
						PPGWQ**PGP*RAPGLQKAPKG
		1		ŀ		PSYQQGPAPPSHRQSTAQRGVR
		1		1		PRTKRCPSLGCGDLSLLSLAVP
ĺ						VAQPAPRCAYRMLPLLFLLGRL
						TPVPSPLSSDKVIYNLHLQFIVF
		L.			-0.4	TSIKFSATPFKKKKK
3446	33814	Α	3483	135	396	LCWLQIHRQGRKPCSPPSLKG*
}						*ATCMPPRRRKGGFLSSVSMDII
			ŀ		İ	THSPGNEKIKMPPPTMSKQPGV
3447	33815	<u> </u>	3484	256	1860	LQQDCREKLSHCLVCSSLG RAPETPRKILGEAGGCRGDGDR
3447	33613	Α	3404	236	1800	PAFQPVRNSRPFLSKLLGQCGR
						STLCRLCFRSLNHLFWLFPGPG
İ						WRGPGGHSTEDGSLQGKAGQD
				İ		FSC*NLEISFFP*PSPTCSPTLHC
			l			GQKPRAGQGHLHSV\PGAPCW
						AEVPALLPRRVGD\PGPDILPPS
1			l			TRV*RCPLDRNSPILL*VHFLKD
l			1			RATTONTARPPMGWRPLOOSR
			l			OISPAVGGKLCSLPVMI*ASPHP
1		ļ		1		SASVVGETPA*IGGWGW/P*GF
l			İ	İ		QLIG/LPHVRGTQPGLLESRVPS
	ľ	l				VRGTQPGLPGLPESRVPSVRRT
		l	l	ľ		QPGLLESRVPSVRGTQPGLPGL
			İ			PESRVPSVRRTQPGLPDARVPY
l				1		VRGTQPGLPGLPESRVPYVRRT
l		l				QPGLPDARVPYVRGTQPGLPGF
		1	Ì			RPSRVPRSFCEGDAAGPPRRPRS
l		l				YVRGTQPGLPAFPSPAFLVRVP
1	l	1	1	l		SLRGTQPGLPGLPESRVPSVRRT
						QPGLPDARVPSVRGTQPGLPGL
l	l		l			PESRVPSVRGTQPGLPDARVPY
1				l	i	VRGTQPGLPGLPESRVPYVRGT
L						QSSLPGLP/GVPRSFREGDVAGP
3448	33816	В	3485	111	258	
3449	33817	Α	3486	μ	4455	<u> </u>

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3450	33818	Α	3487	1	2302	MTECLORFIDSIAAVPRSTKSTV
						QKCLPCLSDGEDKIPDLIAITWT
						PRQGELLEKNVISETGTLLPTPC
						LDTSTKETADKSTSGKTIHQSIK
						TVLKDLSGSIDDLPTGTEATLSS
						AVSASGSTSSQGDQSNPAQSPF
						SPHASPHLSSIPGGPSPSPVGSPV
						GSNQSRSGPISPASIPGQDPGYG
				ĺ		NS/DKSMGHEYSQR/SFLEDRFP
						IAVWWPRPLRLKNCLSVLSYSS
						PSEVTPHPKSESSGTS/SAAQDL
				1		QGCSQDVGQPASSSGGSTREQS
						TSSFIRIVAASSPSSCWKLQVLL
	-					SG/AGGDYSPVLLIGGYSRVCLP
						Q*SDASAATREP/GQNPVPIPP*
						ASHQCHRKEGPPCRQQAGASQ
			-			MLSRD*AKQLKPSSSHTLSKHK
	1					TT/GTRKSLLFGIKKAYNFTNKY
	1					YSELMTQTRPQSTPSIPSPLPLD
						DAGLERSQGNVSASSFMVLGN
						RERGEDTTGAGFGRSRNKEEVP
			İ	ļ		CTIYVGA:ESP/EMC*WMDHT*R
İ						KEGKGGLVGVPCV/SREHLEEW
ŀ						QYQLQR*ISLKTQQV*RRKSEV
						LLGRS/SNTAQACSCWQLTCFM
ł						AGTQRNPQMAQYGPQQTGPSM
						SPHPSPGGQMHAGISSFQQSNSS
			ĺ	l		GTYGPQMSQYGPQDGGGDVSD
						VVMAIDDDGSCHLLGSAVPGA
	i		l	l		VLVTFNLLLIIVVTLQMTEPQFR
1		l	ĺ	l		EYITGDPLESTCRHASLALAVV
						LHQETAMTMITDSLAVVPHSG

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3451	33819	Α	3488	2	1427	EEPSRREPR/PPGHAPGAVAGG
	1	1				AGPMARAGARGLLGGRRPPGL
	1					RL/CARASARVAAG/CGRRRAA
	1					REPPRRRVPRRPAROPRRGATA
					l	AAATTT*WASGTRPSTAAPEPT
						ASAAAR\RLPLLLPRRAAAPRPE
i						PLFQLRHAGLGPDRPAARPRPR
	1	1				HRSAPGPRPRAQPYGRLRCVRR
		1			ĺ	RSAAGDGG/EPGLAFDEVGDRG
	}	1				PPLTAVPAG\ADRASEAAGPPG
	}	1				ATASHPGPTER*QRGRSEPGHR
		1				TEPRITPRSROEAPOORAPGVG
						RPGAPARPAAAGRRDPLSSPEL
		1			i	GCSARRHSSLPCPRRGRPAGL\R
		1				QRFPALEPSPRQPPARAPR\HPR
						TCLRRWTPAPGPRRSTRPLPRR
		1			i	APMPPGPPVARPGP/PPLSHPTA
						RAF/HGTPATRARGPAPVQCED
						A*DLOPAAPRPLRORGPRVPVP
		ı				KDQ*QDRGHRVKRGRGA/RRG
					l	MGWGPVCPSEPQATGRGAPAV
						RPALLSASTAVVSWSLQAAGSS
3452	33820	A	3489	1	262	СК
3453	33821	A	3490	411	1919	RSYGVRWRRHAPPGRRSSPRIG
3433	33021	ľ.	3470	ļ	1777	KVKSASRA WRLRCCGCRRPSR
					į.	TGMRWOMRWPMVTLAROPFW
						RRSVSWRGAWGSWRKSWRRS
Ì					'	RATRSCSMTATASCSCRLSRID
						DISNYEVNLEPGGHDDITSCOG
		1			İ	RGRSLPQRAPIGLCCSLGGGAV
				i		LADTPLFLPRPKPRDGPGSRAF
ĺ						OKROOOOSALRVMORNCAAY\
ľ						LKLRHWQWWRLFTKVKPLLQ
ļ		1				VTRODEVLOARAOELOKVOEL
ŀ						QQQSAREVGELQGRVAQLEEE
l						
ļ		1				RARLAEQLRAEAELCAEAEETR GRLAARKQELELVVSELEARV
1						GEEEECSRQMQTEKKRLQQHIQ
						GEEEECSRQMQTEKKRLQQHIQ ELEAHLEAEEGARQKLQLEKV
						GEEEECSRQMQTEKKRLQQHIQ ELEAHLEAEEGARQKLQLEKV TTEAKMKKFEEDLLLLEDQNS
						GEEEECSROMOTEKKRLQQHIQ ELEAHLEAEEGAROKLQLEKV TTEAKMKKFEEDLLLLEDONS KL\ARLGA*GQLGKWGWGALV
						GEEEECSROMOTEKKRLQQHIQ ELEAHLEAEEGARQKLQLEKV TTEAKMKKFEEDLLLLEDQNS KL\ARLGA*GQLGKWGWGALV G**MVNFTPWGLPHCGSQERK
						GEEEECSRQMQTEKKRLQQHIQ ELEAHLEAEEGARQKLQLEKV TTEAKMKKFEEDLLLLEDQNS KL\ARLGA*GQLGKWGWGALV G**MYNFTFWGLPHCGSQERK LLEDRLAEFSSQAAEEEEKVKS
						GEEECSRÖMQTEKKRLQQHIQ ELEAHLEAEEGARQKLQLEKT TTEAKMKKFEEDLLLEDQNS KL\ARLGA*GQLGKWGWGALV G**MYNTFPWGLPHCGSQERK LLEDRLAEFSSQAAEEEFKVKS LNKLRLKYEATIADMEDRLRK
						GEEECSRÖMQTEKKRLQQHIQ ELBAHLBAEEGARQKLQLEKV TTEAKMKKFEEDLLLLEDQNS KLNARLGA*GQLGKWGWGALV G**MVNFTPWGLPHCGSQERK LLEDRLAEFSSQAAEEEEKVKS LNKLRLKYEATTADMEDRLRK EEKGRQELEKLKRRLDGESSEL
					·	GEEECSRÖMQTEKKRLQQHIQ ELEAHLEAEEGARQKLQLEKT TTEAKMKKFEEDLLLEDQNS KL\ARLGA*GQLGKWGWGALV G**MYNTFPWGLPHCGSQERK LLEDRLAEFSSQAAEEEFKVKS LNKLRLKYEATIADMEDRLRK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first eodon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /=possible nucleotide deletion, \~possible nucleotide insertion)
3454	33822	A	3491	3	266	KMRRLIKSKKDI\NRERQKSLSL TP\TRSDSGEGFLQLPHQDSQDS TSVGTNS*E\DGQTQHPRPI*DA QSSVCCAGSQHGM*ANHSQE
3455	33823	В	3492	1	241	
3456	33824	A	3493		1486	SRI-HIL CNKPRRSGTTINAKRY GPDCHPMGREGAR*HHALRGR RGEAGTRGGRQRRREQDWREA GPOPRAEVGRTAASARRAKGS AFOPRGPSRGSRSWN TGOPRR NGGRGAERRMGGRSWN TGOPRR NGGRGAERRMGRSRPENGAR GGSKDIPAARRRVETCPGPEPRPV GDEPRPWKGGGDARGDPKFP QU-PPRPWKGGGDARGDPKFP QL-PPRPWKGGGDARGDPKFP QL-PRPWKGGGDARGDPKFP QAPNAYDGFCIPAGGVLGAPI AAGLRPTGDVALRRPAGSVEPS GS/AGSQSCLLCPVPYRQTI STGPPPGGWGSPSDVPCSALIS GTGC/PKAQHVSGSLSQRSLSL UDPGRPASRGSLFPWLGTGG KSIPAAPSPQTLWQSS/PGFLYF PGE/RKGKG*GSPGAGCEPPIPA GTKGPRAQRGVQQCTSQ*PSI VWMTSGRGAHSRGGPVRGA SREVPAAVHGGDGLUVECHTA GRVQQPSTGG*PLVEPPAGGR REVPAAVHGGDGLUVECHTA GRVQQPSTGG*PLVEPPAGGR REVPAAVHGGDGLUVECHTA GRVQQPSTGG*PLVEPPAGGR REVPAAVHGGDGLUVECHTA GRVQQPSTGG*PLVEPPAGGR REVPAAVHGGDGGLUVECHTA GRVQQPSTGG*PLVEPPAGGR REVPAGNSGLSSOLSTVLTTFLIF
3457	33825	Α	3494	3	393	
3458	33826	A	3495	145	1089	WYRTEFLODRNYFFLSLVVSAP RTVPGTWTCLLSP*RNE*ILGC SLFPKAGQAP*VAHITLGFQSSE YSKWKFTNSPTFLELLEEFPSLC YSAGFLLSLLPILKPRFYSISSSQ DHTPTAHLTVAVLMYHTRGL QPARATLMSTHSSSHFEGPLPA AVSAGOCASGFRLPEDPSHPRV LIGPGTGIPPFLSFWQQRLHDSQ QKGVAGGFFGVQGGRMTPYFE CRSPNEDHIYGEMLEMARKG VLPAVPTAYSCLPGKPKVCVQ
						DILQQQLASEVLRVLHKEPGHL YVCRAVCMAWDVAHT/L/KQL VAA*LNLN

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ľ	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3460	33828	Α	3497	87	992	TACGFIACIG*QRLEYCY*DHK
						GKQQEVLSKHLQMAMDISHIR
			}			RNVSCSGRNKASSKAYGTGGS
		1				OGRACDLGHNF/TTPSSWERHC
						TLTSQGVDDFLNAKATFKIFDF
İ						SDAFVLSKVGFSGILIQKDENKE
						ELSDKDIYMEAGIFVSANRGPG
		l				VDYCGNRGLSIQGHGGWTLRP
						SILVSPGVEVRGNEDSVDTAAC
						IPAAPAPAPTLAERCTGTAWVT
						ASEGASYRPWLLLHSVKPVSPH
						STSLETWEPPYIFOKMYENAWC
				ł		PDRRLPKKOSLMGNLYLGSAE
				ı		
				ļ		GKYGVGAPTLETTIMQTPDS
3461	33829	Α	3498	1	382	TADCAKPVPLAVVSLDSRYGQ
						WESRSSIHARH*LNSSSSSSSSSS
		ĺ		1		SSPPAVYPRFIEFIHFDIQSTGQK
l				i		SHRVNTRRGP\RDALF*LNSLIP
1					l	LVRTSSKSAARRRP\GEAPRGTA
						VPGADPAGGTRPR
3462	33830	Α	3499	229	367	
3463	33831	Α	3500	233	525	WYFPAGRAGPADPGPGPLAGT
						PGAGAGGLPTYSTPLRVSSPVP
					1	RLESSSTG\SSFPADSAKP\VPL\A
						VVSLDST/RRDSGNSRSFHSWG
						VIN*MTRHLVH
3464	33832	Α	3501	386	729	TGRGCCLPCTWRIRAQTCLT*T
						QCC/SCPTTYPGGGERRERERK
					i	RRGEKEKQKVLRKYKEAMSNK
					1	VCKYFDEGCGSCPFGENCFYKH
				ŀ		VYPDGRREKPQRQKVGTSSRY
1						WAQRSNHF
3465	33833	Α	3502	63	559	HSSTCECT*DSRCGCKWRSAKQ
ŀ						FESKIIKSCPECRITSNFVIPSEY
}						WVEEKEEKQKLILKYKEAMSN
		l			1	KACRYFDEGRGSCPFGGNCFY
ŀ						KHAYPDGRREEPQRQKVG\TSS
						RYRAQ\RRNHFWELIEERENSN
ł						PFDNDEEE/ALSPFELGE\MLLM
						LLAAGGDDELTDS
3466	33834	_	3503	374	656	RRVGCRCFHPSQTGTCT*RPPW
3400	33034	Α	3303	214	030	NVHH*PATCHLAYNRHSWSPH
1		1	1	I		
1		1	1	l		RA/HWHIATAIQLSAHVF/ACHY
1		1	1	l		QQLHHYHQHHHHHHHYRHHH
	L		L		L	ннинниченин

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence	ł	
3467	33835	A	3504	11	11337	MOLOILTIFLDLHHNTNICNELE
	155005	ļ.,		ľ		SSNVDDPCDIWEKVHISLIFTAK
						GSKIPKSSDFQADRELNMFDIIS
					i e	OYDGCPGSIGLTSGAGSTHHRA
	1			1		PWTOTYPOGPTHLSGSPGCILA
	1	1	1			SITGRVTKMPESSESPAWELPRE
	1	l				TELFLSIKDEWTCIFLQLCCPTM
					l .	LLSGFPPIRIEPWSPLSDOLNPIP
•	1					LEAAIATHSRIHHCPLVFTASLP
Į.						GPLTAGNOMADRLVATAVSNA
		1				RHFHNLTHVNASGLKCRYSNT
	1	1				WKAAKAIIORRPTCOKRKIK/PD
		l				QEQPVQPV*AEGVRFWREDH*P
		l				/SHIRSRHSRMTSVSRRQSTWW
ŀ		ı				LPSVTWT/CPTTEALEYGSGAC
	l	ı				LGCPISGVSKGNKTRSGAAGFH
		1				
		1				/SPAFKSALCIWRFKQQHANRP YVCWGMEHRSPYSLLPRSSSSS
	1	1				
	1					HPQIHGNLDSDDLQVQRGECFI CRPCFHRLRSVPDTDTOCPOPR
	12222	-	3505		1158	CRPCFHRLRSVPDIDIQCPQPR
3468	33836	В	3505	35	369	
3469	33837	A	3506		564	PCASRTPVSSPWPV*POPTSARR
3470	33838	Α	3307	345	364	SPRCLPMVQ*AARASHDSQLCS
	ŀ	l				
}	1	i				CRFCVVVTPCAPQGQTCTRQV
		١.		10.5	0.16	CARVTHG
3471	33839	Α	3508	437	946	SFSSKIVQRMSSSCTENMHMSP
						SAPSSPQRPGALSLS/RPSGVGG
	İ					LLKDPIAPC/SR/RLPGILSLSPQN
	ı				l	PRAASPDSPAGFWDSVLCTCRL
						LRVACLCAVRSPRPRLCTRSCK
						GRGSSMVR*GGGLPIFSSSFSAT
1		1				SLQLSSETVARVTPADECPAESP
						LPSHGPVSCQGIT
3472	33840	Α	3509	1259	1497	KSNMSLLMVFSISSGITVTMCSS
		ı			1	WGHLQCRQIFLSLEGLMKTSRS
1	1	1	}		1	GPWAVL/RGWFSHT*ALDEDA
l	1	1			1	ALGHPWASTRKQAPS

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	or peptide sequence	deterior, (-possible nacicolide insertion)
3473	33841	Α	3510	268	1278	SPSGPSSSHQPPALKGQVLQCL
						LSP*ISLRLNLHLWDVYLVEGE
	1					QVLMPMACTAFKV*WSKSTCA
		1				QWHWAFLLCLFFLLFLLDSKK
						DNRPPVLRAGAQCMCTAHVEV
						LPD\PSVFLSAKPRQGSSAARAV
						LASRGRKALCSG\IHVPTPSGLG
						CGGPLVP**FQTELLSSCPF*MC
						PGQPSCPAIPDTLENAVQ\EEAG
		l				PVKAMREKGEHGIPAAQPASS\
						SPGSLVPTCGTVSPSQGTIRRPR
	Į.					GAWPRPQPRLTPLLSAPPWMR
						HLH/RSLWVGTISQEDQLATCW
		1				QANHTVEGAEIGFHCTKPQCGR
						GFAGPQGLGSATSTWNVLSSLQ
	į.	1			1	ASRSIWDTAH
3474	33842	Α	3511	1	1557	MSRISDDCSELCPLKAIKKERR
		1				KEKKQEKWETYRE/REKRQRG
	1	1				QRRRNGERKKRKNTKKR*NAG
	1	l				REGEKKRQKGKTEERKRRGGR
	1	t				RRRETKEEGGS*RNKKQA*SEE
	1	ŀ				KKGRTGKNRKERRKEEGREKE
						RK\REKDRRGGRQKNKTRERD
						WGGEQQKTEREEEWARKRWK
		ŀ				VPGGWEREAPHRELEKNEQLD
			1			KHSSSRAKLYDAGQLDLCSNLI
			1			QSCDPECPMQATSLTRYPTTTQ
			1			IFLRGAQGWVCVELFRSYGVE
			1			DTSAWERDMRNFGCMTREKQ
			1			GKPGQLLAHRHLCAHQKMSLL
			1			CADNSQKGCLSPANAAPCYGV
		1	1			QVAILTSAPTCPYHLEPLCRSFS
			1			LSDQQEAISDPRTAVRIARSGAS
			1			SNPRLCVTLTFPRVLQPFPHPPQ
			1			RWGEATKGGRLPAKGSPARTA
	1		1			AGRCGRSAGMPPDARAIFTSAA
						ALPKSRLVPSNIAFKGKRKDLS
		İ	1			TKAAAPNLLALRYPRPSAPVGG
	1		1			SHAPSPGOOLOPEEEGNEEEEE
			1			EEEGDRAPVFTTGRKDRDSLAE
3475	33843	Α	3512	1	525	
3476	33844	Α	3513	69	707	LRQNQHEVLKDPRTHTHGGQM
		1				GTSSPEQRSTASGAPGWRATSS
		1	1			CVLLASPHHVHHAHGSQEAAS
		1	1			TPPVPWTQREYHGWPPGIYPFS
	1	1				SHLHK/RLLPNPAREEL*RRQQA
		1	1			PWKRHCWRDVTTPESTKNLVE
		1	1			SSMVNGGLTSQTKENGLSTSQQ
		1				VPAQRKKLLRAPTLAELDSSES
	1	1	1		I	EPRTAVHSSCTAHRCSAWCLA
	1		1		1	VSAVCPSRPCOSORGLALS

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3477	33845	A	3514	181	446	TOGGRIKRHLGTSASPTGIMKY
		[ļ-,		PPYCTCPCFQSALHPVPGGLSG
		ĺ			i	KEAESQ*LSPHHPSSQAPGEDPT
		1			1	P/SOP/RLPKHSTLPALGFPATCG
		1				R\SPSPKPALPPRGTAPAPPHRY
						CCYYFPNRSHE
3478	33846	В	3515	58	1034	
3479	33847	С	3516	1	1470	
3480	33848	Α	3517	1	606	MAGEDETPVPLPICGTRPI/DAA
			l			AAHMAPVPSHLRKHQRVEVHG
1					l	FCQVQPSYGPGEDRGLADRGST
1						DEHNPGAAQPRAAALHAHPGG
						VSQLPAPAH*AGQPPPTEPQLP
						VSPA*SNPQVSAPSLSPKQLPSP
				1	1	GS*DPAVPGLAE*K*TNSCPRD
						YTAVAAVLGSAPAAPAQLHPA
l					l	CTLRAPSLRALQEAGAPQPPMG
		L				GSGQR
3481	33849	С	3518	76	1275	LET OF STANDARD A POSSED PRO
3482	33850	Α	3519	1	508	MTRQLSNCWVAAECCDPLRHV
						TQQVLQEAPIVSQAVGGPSRTN
l					I	LATTPGSHRSTYCLSGAVSSRN
					l	LIEPAGEEAGATRARAEEPPGR
						LRAPSGGVPSPRPLCCRPPVAG
					l	CGSGLKMDEDGGGEGGGAVY
						CNLELKASGVILAVAAEKPSSG
						QAVLTNTEHSEPSHLKGKSSEK
					i	SYLHATPKEDIASFIAFLNVYKQ
			ŀ			QGPP*APSYSTL/PPPPSPPPSSSI
						LRPLPQPATGGRQQRGRGLGTP
						PEGARRRPGGSSARARVAPASS
						P/DGLDEVPRRDSSGETVSRTM
		_				AARGCGQVGPAGASYSL
3483	33851	Α	3520	451	487	SPLEKSWPGTSHTWFP*SRP*NP
						GRPLPDPLPADP/LRGVPPPNQR
						KGMSESSRALITPFHPPLTPAPL
		_				*NRPFLWSLF
3484	33852	Α	3521	ı	758	TPRAPLCRGAASAARS\CKWAP
						WPSRPRPRHP*SCAEAREGSAA
		l				QIPPASKLKHGGPSPPAA/PRRG
						HPRLLPAPP/VVPLPATAPAAVP
	1				1	SAPGKPFPTPPGLPKADPG/PIG
			1		I	GPLSAFSGSPPFPVH/EPTVLGSP
					1	QSTRNLPRPPAA*PPVAWARDA
ļ				1		P\GSSPAAAAAKQTFASTQQTP
						KTT*EPRSPTGPAPALAKLFLTP
				1		GTCAPGQPSRKIKLPSRPVAPM
						GTIENIGYITKAFDWNVLFSDTT
		1	1	1	1	KGVRVDCMVQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3485	33853	A	3522	3	801	TLLMSHQKLLPLPQIKTPRSFHH SRHLHHQHRHHQKQHHKKHH HHFYYHH"NHHHHHHCHTPS PHHHHRHHYYHHHHHHPHQH QRHHHPSCTVCPQEE*/HNEHR KRPHRCWKVQDPRNILGYLYIP TTHSELRLALSKHLPSFL*NKVS IYYRQSPDLCPHLNLNPHQYHH RYHHQYHHHRRHKHYPHHH HHLHHHHHNHHHQNIHHHIQE TPLHRTLGLPQGPRRSSAAQP PPPPPPPLSQRPLSRH
3486	33854	A	3523	3	229	WDPPPEFFGRRPRRESSGFPASI LLVTEPGARSPPRPAAHS\HPPS PLHRTLGLPPRHPDGAAAPRSS PPPPPPSP
3487	33855	A	3524		1257	MKABIKMFFETNENKDTTYON LWDTFKAVCRGKCIALNAHKR KQERSKIDTLTSQLKELEEQEQ TPSKASRRQEITKIRAELKSWFF EKINKIDKLARLIKKREKNQI DAIKNDKGDITSDPTEIQTTIRE YYKHLYANKLENLEEMYEFLD TYTLPRIS.QEVESLNRPITGSEI EAINSLPTKKSPCPPGGFTAKFY QMLEVLARAIRQEKEVKGIQL GKEEYQLSLFADDMIVYLENPII SAQNLLKLISN'SKVSGYKINV QKSQAFLYTNIKQTESQIISELP FTIASKRIKYLRIQLTRDVKDLS KENYKPLLNEVKEDTKKWNIP PCSWYGKNIEMMAILREVIKEMI NEPSWYGKNIEMMAILREVIKEM AIPELPMTFFTELEKTTLKFI WNQQRARIAKSILSQKNKAGGI TLPDFKLYYKATYTKIA

SEQ ID NO:	SEQ ID NO; of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3488	33856	Α	3525	2	2133	WRRIYQANGK*KNK/QKKAGV
						VILVSDKTDFKPTKIKRDKEGH
			i			YIMVKGSIQQEELTVLNIYAPN
		1	ł			TGAPRFMKQVLRDLQRDLDPH
		1				TTIMGDFNTPLSTLDRSARQKV
		l				NKDIQELNSALHQADLINIYRII
						HPKSTEYTFISAPHRTYSKIDHI
						VGRKALLRKYKRTEHTDCLSD
						HSAIKLELRIKKLTQNSSTTWK
						LNNLLLNDYWIHNKTKAEIKM
						CFETSENKDTTYQNLWDTCKA
						VCREKFIALNAHKRKQERSKID
						TLTSQLKE/LEKQEQTHSKASRI KSRRNG*IPGHIHPPKTKPGRI*
						VPE*TNNRV*N*GNN**LTNQK
						KFRTRRIHSQILPEHSAGSSGQC
						NOAGERNKGYSIRKRGSOIVP
						CR*HDCIFRKPHHLSPKSP*AVE
						QLQQSLRIQNQRAKITSSPIHQ*
						OTNREPNHE*TFIHNCFKENKIF
						RNPTYKGCEGPIQGELQTTAQC
						NKRGHKQMEEHSMLMDRKNC
						YHENGHSAQGNL*IQCHPHQA
						NDFLHRIGKNYFKVHMEPKKS
						HCQVNPKPKEQSWRHHAT*LQ
	İ					TILQGYSNQNSMVLVPKQTYRI
						MEKNRGLRNNTTHLRPSSL*Q1
						*QKQEMGKGFPI**MVLGKLAS
				ŀ		HM*KAETGSLPYTLYKN*FKM
		1				D*RLKC*T*NHKNLRRKPRQYF
		1				SGHRHEQGLYV*NTKSNGNKS
		_				QN*QMGSN*TKELLHSKRNYH
3489	33857	A	3526	1	1896	
3490	33858	В	3527	1	1296	
3491	33859	A B	3528	1	1095	
3492 3493	33860 33861	A	3529 3530		1413	
3493	33862	A	3531	1	1167	
3494	33863	A	3532	1	1575	
3495	33864	В	3533	1	1653	
3496	33865	В	3534	1	1932	
3498	33866	В	3535	I	2451	

NO:	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3499	33867	•	3536		2502	MTELTOIQOPQIVLFEHKGIIKL VQGSSSDAGKVNRIYOHYESA DKFNYTTGLAWKTAPEQTGKT VRKQQIKLNYKKMESRSKNQGE HESSSPPMEQSWRENDFDELREE AFRASNYSELQEEIQTKGQEVK NFEKTLDEYTRITNTEKCLKEL MELKAKARELREECRSLRSRCD QLEERVSYMEDEMMEMKEG KFREKRIKRNEQSLQEKWDYV KTPNLRLIGVPESDGENGTKLE HTQDIIQENIPNLVRQANIQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAARKEIQTTITR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNEPITGS EIVAINSLPTKSSPGPVGFTAE FCQRKIEGILSISFCEASIILIPKL GRDTTKKENFRPISKTFOTYFT KILANQIQQHIKKLIHHDQVG FIPGMQGWFNICKSINVIQHINR KILANQIQQHIKKLIHHDQVG FIPGMQGWFNICKSINVIQHINR TKDKNHMISDAEKAFOKIQQL FMLKTLNKLGIDGTYFKIIRAIY DGCCPLSPILTNIVLEVLAGAIR QEKEIKGVQLGKEEVKLSLFAD MIVVLENHVSAQNLLKLISNF SKVSGYKINVQKSLAFLYTNNR QTESQIMSELFFTIAKRIKYLDG QTROVKDLFKENYKPLLNEIK EDTNKWKNIPCSJWGRINVK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
3500	33868	A	3537		2197	MNNAKENFLGRFQDGRIGTAP VYSPOHQRRRRRVISALPTEPPI VYSPOHQRRRRRVISALPTEPPI VISPOHQRRRRRVISALPTEPPI VILTVRKITTKQEGISTKTPSVY VHHORKEGENTENGRONGRNGRNGRNGRNGRNGSRNGSNESASSPRECSSSPATE QSWMENDFDKYTEVGFRQLVI INFSELKEDVOTHHKEAKNLE KRLDEWLTRINSIENTLIDLMEI KRLDEWLTRINSIENTLIDLMEI KRLDEWLTRINSIENTLIDLMEI KREMENSTEDOMMEMREEKFRE KKMLEVLPRAIRQEKEIKGIQL GKEEVKLSLEADMITVYLG ISAQNLPKLISNFSKVSGYKINV QKSQAFLYTINNRQTESQIMSEL STHIASKRIKVLGIQLKRDVKEL FRNYKPLLKEIKEDTIKWNNIP ISAQNLPKLISNFSKVSGYKINV QKSQAFLYTINNRQTESQIMSEL FRNYKPLLKEIKEDTIKWNNIP ISAQNLPKLISNFSKVSGYKINV QKSQAFLYTINVEMAILPKJITVRF AIPIKPPMTFFTELEKTTLKFIRN QKRAHIAKTILSKKNKAGGIMK CWENCLAICKLKLDPFLTPYT KINSR WIKDLNVEPKAIKLIEED LGOTTIQDTGMKGPMSKTPKA MATKAKIDKWDLIKLKSFCTA KETTIRVNRQPTKWEKIFATYS SDKGLISRIYNELKQIYKKKTI NSINKRAKDMNRHFSKEDIYA KRMKKCSSKLAIREMOIKTT
3501	33869	A	3538	3	242	RYHLTPPEVEVVLETL/NH/RSW NLEEMDK/VLDTYT/PR.ND/ ESLNRPITGSEIEA IINSLPTKKS GPDGFTAKFYQSIVLEVLARAI ROFEKIEKIGIOLGKEFVKLSLFA DDMIYVLENPIISAQNILKLLSN FSKVSGYKINVQKSQA VLYTN NKQTESQIMSEPSFTIASKRIKY LGJQRTRD/VKDLFKENYKPLLN KIKEDTNKWKNTPCSWIGRIN MKMAIVPK/VIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRARIA KSILSQKN

SEQ ID	ISEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		1		sequence		
3502	122020	-	3539	281	3228	VND, CANALANA FARRADA DA BAR
3302	33870	Α	3339	281	3228	KPRLENYMKNAEASRADAINW
						KKGY/LVMEDKMNEMKREGKI
		ŀ		1		REKRIKRNKQSLQEIWDYVKRF
		ľ		I		NLRLISVPESDRENGTKLENTL
						QDIIQENFPNLARQANIQIQEIQ
						RTPQRYSSRRATPRHIIVRFSKV
						EMKEKMLRAAREKEIQTNIREY
						YKHRYANKLENLEEMDKFLNI
						YTLRRLNQEEVESLNRPIRGSEI
		1				VAIINSLPTKKSPGPDGFTAEYY
		ĺ		I		QRYKEELVPFLLKLFQSIEKEGI
		1		l		LPNSFYEASII
3503	33871	В	3540	295	2804	
3504	33872	Α	3541	83	480	
3505	33873	Α	3542	159	729	PTIVGVVIKFSVCISSPWSHLKP
		l				TFHATSWLADGDTDGCVLYFA
	1					SSCSSYQ*HP\CSSVPEPRYGRRI
		ı	l			GSEFSAGSIVRFECNPGYLLQGS
	1	1				TALHCOSVPNALAQWNDTIPSC
		ı				VAPELREECRSLRSRCDOLEEM
1						VSVMEDEMNEMKREGKFREK
l						RIKRNEQSLQEIWDYVKRLNLR
l				i		LIVVPERDRDNGTK
3506	33874	A	3543	h	1116	MMARGAGVLIRKIYPLNYKHS
	5507.	ļ.,	1	ľ		AVEQVSRAYSFYTQRPVVPEPR
		1		l		YGRRIGSEFSAGSIVRFECNPGY
İ						LLQGSTALHCQSVPNALAQWN
		1		l .		DTIPSCVVPCSGNFTORRGTILS
		1		İ	i	PGYPEPYGNNLNCIWKIIVTEGS
		i				GIQIQVISFATEQNWDSLEIHDG
		l		1		GDVTAPRLGSFSGLTPH/WKLS
l		l				RCMAC/DPSERGLSCTWALVI/H
				i		KMEPEOPVCGKOHPEDSOGR/K
				!		GPGPGPONHLLLPGF*VSDGRG
		1				RSRSELTPAGSFQWQHSPRNGV
				ŀ		
			l	ŀ		*LHQPSPAQVPQRLFKWRLLCP
						QFP\GDFVKYQCHPGYTLVGTD
1			l			ILTCKLSSQLQFEGSLPTCEATP
			•			SSQCVWVSPHRPEARLPAHGPA
		_				PKRHVCQKASLLICGKEGMQL
3507	33875	Α	3544	373	1051	RHLLGAQCLSRAPWCWNNQAS
1	1			l		FPFPRCPRAKGQGTARASFSWL
			1	l		GCRIQHEGPIRVQGRRRPHRRE
	1	1	1	l		PAWAHLHPPMPCRQPNLRP/PG
	ĺ					SLRVWPC*KSLC*PSPRPARTHP
l		1		l		PGQRCHPYRVPSPPSPSPRPPS*F
l	l	1		l		SRTFQPPGGPRTLTSGPRTQETL
		1		l		SPENVPGPGAP/PAPRHRSSGPK
	1	1		l		ADVALRMRGLSRAPPSAARKE
l				l		RGSPESERPLNLSDGSGCCKHF
		1		l		TTVRA
		1				

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	ı	09/540,217	codon for peptide sequence	of peptide sequence	deletiun, \=possible nucleotide insertion)
				sequence		
3508	33876	Α	3545	1	411	RGREARNAAAVGAAQACT*FH
		1			1	RTOGPSRLGGVRGQLALPLRA
		l				GLGDCIFPV*AKSEFS/HSPLHAP
		1	İ			ASLCWGP/PPHPVL/WATHRRQ
	1					DCGTLILQGSPAVSN*DSAPPAL
		l				ACRLSCGGGQGERTAPPSRCGE
		1				KTPWEVPG
3509	33877	Α	3546	107	550	TFQMNSLTECCPSLRGWGAPQS
	l	1				LPMPALQTPGSAHLRCQGLLSV
		1				ETEVLWCHPTVIQSAVALKLH*
		1		1		AISPCF*LPPNYPLSGSSL\PTPH
		l				ACLSLPNLQCASPL*QPPPCPRE
		l		i		VAPLSLEIPESFVYGILGTHITGC
						LCISLVLPLSP
3510	33878	Α	3547	54	825	VGGCLAGPQDPDGVFQTSLRK
				Į.		GVNRAQQQRRQLLPGPTPSKA
	1	1		İ		KDSHP*EGG*GASPNAALLSGA
		1		1		GELPRACQCRLSRHLALPTCAA
	l	1				RVC*NPVKPRKGRSEPRSGWAS
	l	ı		l		QLPGGDSRLPLRPGTSQGVFSP
	l	1		1		HRLG/EGGKLVLGVLSLSLKQR
		1				GFPGE\WGAAVLSPVRGPRTGW
		1				GE\DLPRALPDQSDGSGRMRKS
		1				AAEAETGPGARSAAGRSDSDS
		1				GGRPDSCQTVPAAR/SPPCLRRQ
		L.				KLPRERLPRAPNP*GPRPLGR
3511	33879	A	3548 3549	1	1335	MD I CYLLYL CDYNGUETDGGDA
3512	33880	A	3349	'	903	MPAGYHVLSDVVSVETPGCPA
1		1				EFLNIRIPPGDPVFDPDQRGDVP
		l				EPPRRVPPPAARRPIPSTTQGLR
		ı				SVGARCGTGKQLHLQPQCEIH WVKPAGLLSLVGTWRTFMSSS
	ŀ	l				
		l				ELVNIPIGTRYLAQAVTLTVKV
		1	ŀ			CSFTAEASETTSPPGGTNNSRR AALRAVTLTAKVCSFTPEPARP
		ı				
		1				RTHQKEETPNTSEHQKEQTPDT
ľ		1	l	l		SAFKNCNTHGEGLQLHSLSPGR PPTPPGRPNNWRNPGLKSWNT
		1		1		YPGKVRNFHWLFSKKEIEDIRN
		l				1
		1				TTLRDVLVAVINIDPSALQPNVF
	1	I				VWHKGGFLP\CPQFFP

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		ŀ		sequence		
3513	33881	IA	3550	lī .	797	ATREGONLVLVGLGFEMTTVPI
		1				LHAAIREVDIKGVFRYCNTTVT
		1				LTAKVYSFTPEARETTNPPGGT
						NNCRNAGLRAVTLTAKVRSFT
						AEPARPRTHQKEETPNTSEHQN
						EQTPDTPPLGTVTLNARVRSFIV
						EVNSQNPLLMWAAPDPAPGQN
				l		GPRGLYAFGAERGNREPFLQAL
				l	'	GLVLVRLH\NLWGQRLARQDP\
						DWE\DEELFQQP\RQRVIATYQI
						TSPHTCTYSRTRCFPVKEIDKEQ
						SLTSHHYLSCSHCFGHEQSDHP
3514	33882	A	3551	23	3990	HGHFWLGHGPLWLSAPSWTLI
						LENTTGSRGGIVWGTRCPRKRA
						KSSTSPVQSLELRTPFRGRCSDL
					ļ	MGGTTTSWSTDG/CSKGYHVLS
						DLVSVETPGCPAEFLNIRIPPGD
						PMFDPDQRGDVVLPFQRSRWD
						PETGRSPSNPRDPANQVTGWLD
						GSAIYGSSHSWSDALRSFSGGQ
		l				LASGPDPAFPRDSQNPLLITGPG
		l				GCTQRGNREPFLQALGLLWFR
		İ				YHNLWAQRLARQHPDWEDEE
				ļ		LFQHARKRVIATYQV
3515	33883	Α	3552	2	663	VLLDERSAALDGAKRDGTLAL
				l		AAGALCREARAAQVFFLKGGY
		1				EAFSASCPELCSKQ/INVSANCP
		1	l			NHFEGHYQYKSILCGMTTHKA
			i			DISSWFNEAIDFIDSIKNAGGRV
1						FVHCQAGISRSATICLAYLMRT
		ł				NRVKLDEAFEFVKQRRSIISPNF
		ļ.	1			SFMGQLLQLESQVLAPHCSAEA
l						GSPAMAVLDRGTSTTTVFNFPV
						SIPDHSTNSALSYLQSLITTSSHC
3516	33884	Α	3553	3	669	GYEAFSASCPELCSKQSTPMGL
						SLPLSTSVPDSAESGCSSCSTPL
		l				YDQVSRCPCHREEVRTGKGME
						E*CQGGI*KVTCSIIYNGGDTGI*
		1				FIPQLSGLTEPSLQL*ALRK*TC
		İ				WSCPGKWA*FPIYLSSSNRTEFT
		l				RYLKLTFPAESFCGYGHWPWL
		1				*ASLMNVGYFWISG\GPVEILPF
						LYLGSAYHASRKDMLDALGIT
		L				ALINVSANCP\NHFEGHYQYKS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
3517	33885	A	3554	3	1377	WAVCATRVGGAVGGTAKKPR SPEPRVTLLSQSKSGFWFGAER
						PGGLAFPRKAPPCPWPREQTKS TAGPITLGALRPAMVMEVGTL
						DAGGLRALLGERAAQCLLLDC
						RSFFAFNAGHIAGSVNVRFSTIV
		1				RRRAKGAMGLEHIVPNAELRG
						RLLAGAYHAVVLLDERSAG\LD
l						GAKRDGTLALAAGRA/LCREA
		l				RAAQALLPSKGGYEA\FSASCP
						EL\CSKK\STPMGLS\LSLSTSVP
						D\SAESG/CASSCSTP\LYD\QGG
		1				PVEILPFLYLGSAYHA\SRKDML
	1					\DA\LGITALDPNVLSQIVPNHFE
	1					G\HF\QYKSIPVE\DNPKADISSW
						\FNE\AIDFIDSIKNAGRRVFVHC
						QAGISRSAT\ICLAYLMRTNRVK
						LDEA\FEFVK\QRRSI/LSLPNFSF
l						HGASLLQFESQ\VL\APHC\SGR
		ı			1	GWGAPANAGLDRGTSTTTVFN
						FPVSIPVHSTNSALSYLQSPITTS
3518	33886	Α	3555	450	719	
3519	33887	Α	3556	63	332	
3520	33888	Α	3557	573	1309	WCKGEGEATEKGPRAEAQASP
						LSEEAGAGRCPGCPYRDAQPLL
		1				GSGHTLKRAIQDICYGPGHYQA
	1	l				RAAREVHPPGRKIGKQSLRRPC
i		1				KLETDDHLSRSLRELD/SW*FGR
i		1				KCAGAGLTERTQGRLRRKRTL
		1				SSEGALPQVLELSAEASKRGSL
				l	1	GKPRKFGKKNPGHGAPQPVVF
				l		QSRQCLQRILGEHPRTRPCLRN
		1		l	1	DNPGASSAPAQATFISPSEDFSS
1		1	1	l		SSQARSPALSLSFREGLVMTHG

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3521	33889	A	3558	1	1797	KDSAGPGPPVALLLPGAA/CLSP APGCRRAAPRWSSPGPRTAAG* RRMWCASASLA*SPCRPPRSRW
	ŀ					WRDAGSGWTPHCPASAAWGA
						EQEPVRSWGPRASQSHCPGGLR
						APPPGSVRCSTQ*DCSSVRPAW
	ŀ					SRS*GAC*QV*PRCPCRTPATG
						WAPPPOGRCGPTTAPGSTGPAG
		1				RASLCCPRRAHLPG*WPOKLIC
	i			Į.		AHPGAKSLGLACOPHRG\KGTP
		1				IEG/PACGT*GGRRGSGCPGRPH
				i		TRRRC*PPAPCGRRSAGSAHPA
						RPWPHGPGGOORDPGPAYRGG
						OGGRSPASPSGRRLPASRAGRS
1						RAARGTPGRPEPRSPORRTGTV
						QPARCPWPPHRAAAGPPRRGS
						GAPAPLGRTRSFGTAGKAHPW
						PRRRPGHW*SAAAAPATGVPA
j.		ŀ				CRAGSWVSAAPPAEGRPARAR
						RHPGRCPEASGPRGRRSAAHGH
		ŀ				GARAGSPQPGAPPCHLPGIPAR
1		ŀ				OPLGLPRRTRCFGGIAORGRAA
						RHCLLSRPSAKAKRNSSYREPG
		l				MGGWRSPQALGEYGKGSQAG
		l				SARLSGAASQGRRARHLRGKA
		l				PAWNPAPPPSPPPPALGLPLRTQ
	ŀ					REATRKPRREEARRPRPRPLRP
						GGANGSPGPPRAARA
3522	33890	Α	3559	1443	1871	PFVYTSSLGRPPSIS*QPFVSGSG
		ŀ				CSCP*RSRPSGAWRA/RSASSPA
						PPP/KAP/SPRPGPRATAGASRRT
			İ			AGPALCGRPR*GSRGRHLFSRP
		l				GGTRRRRRAAR/SAGLPAPGGS
		1				EPPKSGSGFPSSPYASSSGLIPGN
						RSPAAAGEL
3523	33891	Α	3560	62	864	ALAESRGDLEAGPSSNTWEFW
						ELAGFSVLFLGNRRAALGLCEL
		l		ŀ		PSLRAGVEFTAVQRLWSSAGA
						TWWSKLAVPLAGSAGRENPGS
		l				LLDGLLFTLENNLSRGQGAPST
1				l		PPAARRAAR*DGGQSASSS\PAL
			1			ESPPERHRRLALVSEQKPQEPA/
1			l			RSSRRSCGTRLPRLVFCSKVCR
1						RAEPGGSVTRREGGAEREAEER
		1				KRGR*GEARR/RQGGRKSTRRK
1		1				KQAIKGKRESQKRRGGRQGRG
1		1				RAASPPL*EPRARQPRGSAAPSL
	L			L	L	LRGLSGCL

SEQ ID NO:	of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	location of first codon for peptide sequence	eodon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3524	33892	A	3561	3	2701	TGLWCKCPRSARRSVGRRGGT APAARPRPAAQKQALGSREEV GTGPGRILRPGGWGCFPIGPRGT EDADQRAARGPVGAGTQQHG RAVPRIGPQNEPDETLLP/GGPS PRGGELRGRSGARGLP*SLTGP APGPQRGGG*PSPFGRASSKAG PWKRPGASRASLQRASSN/PAS QVDWGG/PGGSPRCNECKERKP GTGPGWPPRERSPGNLRFGVGG LGLALPARTAAAAPRPRERWRS
3525	33893	Α	3562	2	905	PIGAPELGAQ*PSL HEGEFFFILGCPFPNFIPPNLVSV RKLGVKPAWGAA/RPRLPLAP MPSREGAARSREMRRRGIRRS PKEGLFHPEGSGGKSQNGADPQ RM*REPGSSKSSEPLPRLLGVH OTA*RWETGETGPAIGGPAELD AVHVGL*CNRGFPSSKQRARRR ARVWPQPKKRPPARAARMARL ASDQRDFSVSRKAGDGRFPVIG IRSGGGAATGSSSRLSVSSSAVL RKPGRTTGAVPAGGSARKGPSL APMLGPGSVRSASSPSPGIHPG AGS*ERAGLGERPRQKPLAVPA AAIDFPGSPARSNI
3526	33894	В	3563	149	283	
3527	33895	A	3564	269	452	AGILFLSSSQ*SNARRPTHGALL GDWGPRCSPSPYANRSPSSSLA RQCRTRGSTRDLRVRT

333

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	eodon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				scquenec		
3528	33896	A	3565	ı	1877	MDPQLERQMETTQNLVDSYAA
						IVNKTVWDLMVGVTPKTIMHV
		l				MINNRHAPPHGSRGLLWHWGC
						RWPCWPGGDAGQPYGTSILIEK
						KREKNQIDTIKNDKGDITTNPTE
						IQTTIREYYKHLYANKVENLKE
		i				IDKFLDTYTLPRLNQEEVESLN
						RSITGSKIEAIVNSLPTKKSPGPE
						GFTVEFYQRYKEELVLFLLKLF
						QSIEKEGILPKSFYKASIILIPKPG
						RDTTKKENFRPISLMNIDAKILN
		1				KILANQIQQHIKKLIHHDRVGFI
						PGMQGWFNTRKSINVIQHRNR
						TKDKNHMIISIDAEKAFDKIQQP
						FMLKTLHKLGIDGTYLKIIRAIY
						DKPTANIMLNEQKLEAFPLKTG
	1	l				TRQGCPLSPLLFNIVLEVLARAI
		l				RQEKKIKGSLQRVLSFLTTQRG
		i				LRRSLQPSIPFSFIILVRAMFLLS
		l				GLVAVTLGSPSAGNQSTVLSSW
		l				SLVAQQEKAVPTLPLQSARPPH
		l		İ		GSAVQAAVWPDTLYQSCCPLA
		1				ENQTHFWMTGKCVLCWLCSL
		ı				WSSGEGKGQAISRVLFGGVKRP
		1				YPFQGTLFLESPWNLAGSCPVK
		1				PALATRGQG*SSAYSTEPVIVQ
	i	ł				RNAT*LKGKARVQLGAKKESG
3529	33897	Α	3566	770	949	IRYVLCGGALR\MELLTKQG*SS
	1	ł				AYSTEPVIVPRNAT*LKGKARV
						QLGAKKMMSQSVTPD
3530	33898	В	3567	507	1436	
3531	33899	Α	3568	43	421	TSAHPGGEAVPS/LTTSTTWSRS
	ŀ					SSLVTFTLMPPRGCSTGPPVTSP
		1				LCRMPRTTTMPASPVGSSIGQT
	ľ	l				STTLPSCPQRQT*PSACTGSG*A
	1					SAVRCAPKSSSSPATSSSMTTTT
						PGRATTTTTQTRC
3532	33900	Α	3569	210	610	TRKSRRNG*IPRHIHSPKTKPGR
						S*ISE*ANNR\TEIVAIINSLPTKK
		l				SPGPDGFTAEFYQ\STRRS*TTT
				1		MPASPVGSSIGQTSTTLPSLAPR
			1	1		QT*PSACTGSGNHKSLTVKSFS
	1		1	1	1	OGCAGLPASLTGPLWWRC

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	detection, v-possible nucleotide insertion)
3533	33901	Α	3570	1	718	MENAGEREDPTVGNEGEVRLA
				l		GPVLRTQDELSWEEDEANPTSY
				l		PKGADSYCHSDCQTIMDFSNFN
		1		l		AFSTPNTFALMNTYSCPQHPNS
						KQFQLPTFVKMGEAVSVFFIGL
						PHATPIVEHQNDLIAGSVRMQN
						QPKGSTLQCIILMPQRPPGQTLE
		ŀ				DMDYYYSCFSDEKNLGTKKLS
		ļ				SFPWSHSKEVKATFKGRYPGSF
						ALNRHTTLPGTAWILLLGGELA
						FLTVKDGSPLALPSRPADGMRC
		1				RNKARVLSSLNLTASWG*QAQ
					ŀ	SSELRTSSPGKRMKQTQLLIQK
						EQILIVTRIARP*WIFPTSMHFLP
						QTHLLS*THTA/VPQHPNSKQFQ
						LPTFVKMGEAVSVFFIGLPHAT
				l		PIVEHQNDLIAGSVRMQNQPKG
		l				STLQCIILMPQRPPGQTLEDMD
		İ				YYYSCFSDEKNLGTKKLSSFPW
						SHSKEVKATFKGRYPGS\QPLT
						ATPHYLALPGFSF*VGNLHSSQ*
						RMEALWPCPPAQLMG
3534	33902	Α	3571	719	1643	IQKRACSVSARRGLRTGRCGCT
		1				AGTTTMPASPVGSSIGQTSTTLP
						SCPQRQT*PSACTGSG*ASAVR
	İ					CAPKSSSSPATSSSMTTTTPGRA
		1				TTTTTQTRCASTPPSPSTPGAAT
						AAGGPLVQGHGRHRVRVQSES
1		l		1		HEGHPHGMRPQPHCSTSSTGM
1			l			SAGPRVPGQV\ASSRMLTHTNG
			1			LRGPGGFKLPSHGVLDLQNGT
	1					GMPGGAVCCSTVRGPATGPAQ
	1					TGQRREPRPTRCPWSSVPPLRR
		ı	1			GKKDLARRQVESKPVWPGPWE
		1				GTPWSLLLGCNLPALSLCCIGTS
2 4 2 5	22222	١.	2570		022	ADRSFRKFYFFQTRIPLLLTDVL
3535	33903	Α	3572	1	933	MPEPPP\PPWAPARPKPPRRAPP
		1				PAPRRPVPSTTQGLRSAGT/PAR
1		1				DWQAAPPAALSSPEPHFNLIAS
	1	1				VQTVMCPVGAPAGMQGSG\PK
	1	1	i			PSGCRLVLWTPG**KGSIWGTA
		1				ASMTRRRWTMRSRTAMSPGPQ RVPSAPKPSSAPCA*MEGKRSL
		ı				
	1	1				LPA/TVPGCKKRYKVTWVAVG
		1		I		GPDPTREASLCQPSLLGTDQDL
		1				QSSPFHWHLRIRQKMRYRTPRP
		1		1		HAEQGMGEGSHCLMSEHHFEK
		1		1		TQRQFSPDYYPNPSSQLNVNGI
		1		1		KYHAKNGHRTQIRVRKPFKCR
	1	1				CGKSYKTAQGLRHHTINFHPPV
L	1	1	L	L	L	SAEIIRKMQQ

SEO ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide		in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
ĺ	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
		<u> </u>				CLSLPTPPWTPVRPEPPRRAPPP
3536	33904	Α	3573	2	316	
						ALRRPVPSTTQGLKSAGARRGT
						GRQ/PPPAAPDCVAQ\SSTVHLA
						ARATK*PSAHSVVSSSPMGVLF
		<u> </u>				LHGLDFPRMTRSQGLR
3537	33905	A	3574	3	1078	SLPPPPWAPVRPQPPL*VPPPAP
ŀ		1		1		RCPVPSTTQGLRSAGA/PARDW
						QAAPPAAQVFTLLKNIKMLPCL
	1	1				EKPGKFGSLVIMREFNNHMWQ
						VELKMPVPSDLPKGTGKTLILP
	1	1		i	ŀ	ECIQAPCMKSNNA\PSSSSAPSP
						WML*A*AWLCRYCRASCGISSI
						PTASPVTMACC*RYMRWGILPI
ļ		ļ.	İ			SEPP\QTGFSPAGANQRGPLAAT
	1			ŀ		LSGPGGEGQSAVARLTGEKKN
		ļ	1			HPGAQYANRLSPRVGRFINAAG
1		1		l		TTGFPTGKRAGHKKEPIPQSFIT
			ł	l		RAARRSR*PSKASELGRKQRRP
	1					V/PVR*LLRSAQEEISAVGKTPG
		1				FCQGGNTGYQSQR\RKK*PANR
	1	1				PVKRLP*GGI*SLPGSKTYAVSV
	1			1		RCPDQKI
3538	33906	Α	3575	2	969	VSTWETPQYRRPPSPS*RGSREQ
1						PCSFSSPRDTPGENHWLSLPQR
						D*AGPPVRRALGAS*PHATRRP
						NRGGAS*PDLQPNHTRPFRPFPS
						KNPCFRFPEPLRAPTLVPGPCKP
	1					HSPAASGRVPPTHPGRGLGKSE
	1	1			i	G/SKEKPMRRTAAPTPIRFPKIT
						GT/PSTQTAADHALLGMRDQSL
1						SGQSPGPKSPDADDQLQNRDH
1					1	TETEQRISSGRSSALAPESQLQQ
					1	GCAGIHFRGRFCKAPPLVCERL
					1	RGW\PRGKRKGVCESAAQASP
					1	MSAAPCSTVPSPINHPRAEECG
					1	RTARDWQAAPLAALVRDPLDE
				1	1	ASWAPESGGDVENLYV
3539	33907	c	3576	ī	444	
	1	<u> </u>		1		L

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequenee	l	09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
			P.	sequence		
3540	33908	Α	3577	227	2141	FCPVATSASVTPVQTRCATRPT
				l		TAPSADCVSPRAAGGLPSGHCF
1				1	1	RSEP*GKNWAPCPQPALTPSS/P
						SQTSDSEEHPSSENIPPGYEVVS
				1		LLEALNGPLTPSPAVPPLHVL/E
		ŀ				RWPPLRNAPFIWQ*WPPAPRQD
		ŀ				DLAS*PPV*/PAAVRDSNSKRVS
						PNPLPKTLPCCMKRKMSIPAAS
ľ		l				TETQLSQRPSVQHLGEECGVTP
						ESENLTLSSSGAIDQSSCTGTPL
		1		1	1	SSTI\PPQKALPAAAWPSLSCPW
1		1				HPPRSALTPSPPCLAPTSPLALK
			İ			RRERLSLPPSLPAGPPQKK/REG
1		1	ļ			LPAESPDSNFAGLPAGEQDAEA
			1			ALSSHYQPISHASKGDCKSGME
1						QQGVCEREWGPATVQSDTPAA
						AVGLAAPGRQAVEGLSVCSLR
						PPCSSRCDGSGCSGQPTTVINIS
ŀ						LRRPTSPRTREDSEKPGQYPKG
		ĺ				HTEARQMPGQKDKVAKRSRK
						V*EEKENGKGPIRRQ*KQAAPR
		ĺ				QLGQAGLTHSLKARV/RGGTG
1					l	G/AAGVLG/GAWAWRAPHQW/
!						PGLIALPARGNEGLSTRASGCG
1						GCTGSPSSASPPALRSISRRALA
1						AFPRGRARDLQPAMPEPPTPSV
		1				GSCAAPASPMSAAPCSTA/LQS
		1				HRPPKG*GVRAHGAGLAGSST
						CSPSAGSTG*S*LGS*VWWGRG
						EPLCPAQGL
3541	33909	Α	3578	26	1141	VLQLLRWRVWSLFFLMFRCVR
						SFFLLTQKPSWLHPVDPAPGLQ
		l				VELPASPAPCARTPQPLGGRWD
1					1	WAPWSRGRRSSGRLGLHRNLR
1		1				RPGAQAWRAAGPGPCPAGRQL
						RPGEKSSAAPVGWHCWGTEYT
1						FPSSRWPGC*APHCPGLAGPAG
1						SPSAGPAKPTPTWNSSWPASAA
						RSPGSYS/PPLPPY\PLQAEGAGS
		1				GLGQPRKGLLHL*DVPAEPVLA
1			1	1		GPLASGSIPLAAPPAGRGLLAPG
1				1		PCPGLDLRLL*QLPPPSVFPTTP
1	1		1			KTELVLGTPGHGQPHRGGHESS
1	1			1		DSAGG/APTPRALRSGWDPSPPS
1			1	1		SVCATPTSSGLSSTPQLPLHQRT
1	1				1	SSSTASWSPGWGMGSC*VLVTS
		L				GAATVGC*RLPSISTS*SPI
3542	33910	В	3579	1	1234	
3543	33911	Λ	3580	443	865	

AISKAPARJIEPALRGHSÖSRGG TPGGSSALLCAKNCAPGDPGT	SEO ID	SEO ID NO:	Met	SEO ID NO:	Nucleutide	Nucleotide location of last	Amino acid sequence (X=Unknown,
	NO:	of peptide	hod	in USSN	lucation of first		
		sequence		09/540,217		of peptide sequence	deletion, \=possible nucleotide insertion)
RAPPPAPRCPVPST/TPGAEERG RTARDWQAAPPAAPKEETPNA SEYQKEQTPDTPPLRTVTLTVT VHGFILEVSETKNPPIPDTGLQV VPKPLPRHTRGRYASSSHHIPE PVSPSARAG/APPGHTPCQGTW QIQSSPAQGGAPNPLYSAGSA LVSSLVLVLQVPPVRSPEHS VIARPSPARPGTWELGRRTRP SQDPPRGPSGGPWGRGCPW RSKTDAAPGKA'ARSPAPGASC ELARRGASPGKEGLA'VGRAGA RGVASG/APSPAGEPQAGALGAP PGTHRSSSPAQVPSSGARTESP W*P*PLLASAGRPRPQFOYHAGE GPKPLAGGGBTA'PFAPAPLEPLSAP RASGSFETSTSAHDPGSSGHPW GPKPLAGGGBTA'PFAPCAGCRGS AJSKAPARHEPALRGHSGSRGG TPGVGSSALLCAKNCAPGDPGT AGVOR*SGTQLPPRAPLEPLSAP RRVRPVGGRRREKVPRPGRR AGVGR*SGTQLPPRAPLEPLSAP RRVRPVGGRRREKVPRFGRR GPKPLAGGGBTA'SGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG					sequence		
RAPPPAPRCPVPST/TPGAEERG RTARDWQAAPPAAPKEETPNA SEYQKEQTPDTPPLRTVTLTVT VHGFILEVSETKNPPIPDTGLQV VPKPLPRHTRGRYASSSHHIPE PVSPSARAG/APPGHTPCQGTW QIQSSPAQGGAPNPLYSAGSA LVSSLVLVLQVPPVRSPEHS VIARPSPARPGTWELGRRTRP SQDPPRGPSGGPWGRGCPW RSKTDAAPGKA'ARSPAPGASC ELARRGASPGKEGLA'VGRAGA RGVASG/APSPAGEPQAGALGAP PGTHRSSSPAQVPSSGARTESP W*P*PLLASAGRPRPQFOYHAGE GPKPLAGGGBTA'PFAPAPLEPLSAP RASGSFETSTSAHDPGSSGHPW GPKPLAGGGBTA'PFAPCAGCRGS AJSKAPARHEPALRGHSGSRGG TPGVGSSALLCAKNCAPGDPGT AGVOR*SGTQLPPRAPLEPLSAP RRVRPVGGRRREKVPRPGRR AGVGR*SGTQLPPRAPLEPLSAP RRVRPVGGRRREKVPRFGRR GPKPLAGGGBTA'SGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2644	100010	+-	2501	10	11624	CLCL DCDDD DDUDW 4 DVODCDD
RTARDWQAAPPAAPKEETPNA SEYQKEQTPDTPPLRTVILTUT VHQGILEVSETKNPPIPDTGLQV VPKPLPRHTRGRVASSSIHHIEF PVSPSARAGIAPPGHTPCQGTW QIQSSPAQGGAPNPLYSAGSA LVSSLVLVQFVDPFVRSIPSHS VMARPSARAGTWELGRRRTRP SQDPPRGPSGCPWPGKGRCPW RSKTDAAPGKAMKPSAPGASC ELARGASPGREGLAVGRAGA RGVASG/APSPAGEPQAALGAP PGTHRSSSPSAQVPSSGARTESP W*P*LLASAGRPRPQGAVHAGE WRKRRRPVRTKRFPTKAPAR SAGSFETSTSAHDPGSRGHPW GPKPLPAGGDRTAPPGAQGRGS AISKAPARHEPALRGHSGSRGG TPGGSSALLCAKNCAPGDPGT AGVOR*SGTQLPPALFELSAG RVRPVGGRREKVPRPGRPR RVRPVGGRREKVPRFGRPR RVRPVGGRREKVPRFGRPR RVRPVGGRREKVPRFGRPR QLGVAKSMEGYOSRRDQGGR QLGVAKSMEGYOSRRDQGR QLGCRGGCTAGCR QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGTAGCT QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGTAGCT QLGCRGGCTAGCT QLGCRGGCTAGCT QLGCRGGTTGCT QLGCRGGTTGCT QLGCT QLGCRGGTTGCT QLGCT QLGCTAGCT QLGCT	3344	33912	A	3381	2	1324	
SEYQKEQTPDTPPLRTVITITY VHGFILEVSETKNPPIPDTGLQV VPKPLPRHTRGRVA SSISHHIRF PVSPSARAG/APPGHTPCQGTW QIQSSPAQGGGAPPNPLYSAGSA LVSSLVLVQFVDPFVRSIPEIS VIARPPARPCTWELGRRTEP SQDPPRGPSGGPWPGRGPW RSKTDAAPGKANARSPAPGASC ELARRGASPREGLAVGRAG RGVASG/APSPAEGHQAALGAP PGTHRSSSPSAQWPSSGARTESP W*P*LLASAGRPRPQPGVHAQE WRKRPRRPVRTRRFPTKAPAR SAGSFETSTISAHDPGSGGHPW GPKPLPAGGDRTAPGAQGRGS A/SKAPARHEPTAPARDFGSGHPW GPKPLPAGGDRTAPGAQGRGS A/SKAPARHEPTAPAPLEPLSAP RRVKPVGSGARREKVPRCORRY CYSCMETNLTVSQVKVHEUTV* GPREGATKPNRMKGKEGRSGS LLGEGPFKDESVMSQGSSKD LLGEGPFKDESVMSQGSSKD GEKRRGAQRWKWPMQGICR QLGVAKSMEGYQSRCDQGGG GVSDKWPQVCAKKPEFVPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPASSMAMLAPDPPGQ KQNLSPKVNDIITDIESSSSGAA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPKPRC 3546 33914 B 3583 1 503 3547 33915 A 3584 I 787 MIKWVSVQGCRDGLTYGWSCS VETVRWLPEVHAADTSCLKISA CLSSFSSYKAPSVVAQAAPPSS PHKTSSLCTTSAPSRPSMRTTS APP*USSAARPSI*NISSSPESSAA TI*N*NMSSEGLQLHDTOTRTS APPRVLNSATSGOTTTSAPPRAR TPVVPGGPARPSUNNFITS APPRVLNSATSGOTTTSAPPRAR TPVVPGGPARPSUNNFITS APPRVLNSATSGOTTTSAPPRAR TPVVPGGPARPSUNNFITS APPRVLNSATSGOTTTSAPPRAR TPVVPGGPARPSUNNFITS APPRVLNSATSGOTTTSAPPRAR TPVVPGGPARPSGNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*TKAAPAPPQGSISTTPDLN SGSTTSSSRSSAAPRSI*NIPSEN SGSTTSSSRSSAAPRSI*NIPSLN	ŀ		1	į.			
VHGFILEVSETKNPPIPDTICLOV			1				,
Pyekplerhtrograssishhire			1				
PVSPSARAGIAPPGHTPCQGTW	1		ı				
Qiqsspaqgagaphyriysagsa							
LVSSLVLVQPVDFFVRSIPEIS VIARPSPARPGTWELGRRRTRP SQDPPRGPSGGPWPGRGRGPW RSKTDAAPGKAVARSPARPG ASC ELARRGASPGREGLAVGRAG RGVASG/APSPAEGPQAALGAP PGTHRSSSPAQVPSSGARTESP W*P*LLASAGRPRPQPGY*HAGE W*RKRRRPVRTKRFFTKAPAR SAGSFESTTS-ABPPGSGPHPW GPKPLPAGGDRTAPPGAQGRGS ASKAPARHEPALRGHSGSRGG TPGGSSALLCAKNCAPCDPGT AGVGR*SGTQLPPRAPLEPLSAP RVVRYGSGRREKVVPRGRRR RVVRYGSGRREKVVPRGRRR CYSCMETNLTVSQKVRHEVTV GPREGATKPRMKNGEGGRSGS LLGEGDFFKDESVMSSQGSKD GEKRRGKAQRWK WPMQICR QLGWAKSMEGYQSRRDQGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSYTSCGSYTTOLCHOLL RRLEISPARSNAMHLNPDPPOQ KQNLSRYVNDITDIESSSGGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPRC SSSSYKAPSVYQQAPPSS GLSTSSSYKAPSVYQQAPPSS HKTSLCTTSAPSRPSMRTTS APP*SSAARPSI*NISSSPESSAA TI*N*NMSSSPGLQLHOTGTRTS APPRVLNSATSGUTTSAPPRAR TPVPPGSPARPSGNSHTISSYPESSAA TI*N*NMSSSPGLQLHOTGTRTS APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTSY APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTSY APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTSY APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUTTSAPPRAR TPVPRGSPARPSGNSHTISTST APPRVLNSATSGUSTTPADLN SGSTTSSSSSSAPRSLNNPFS** VSSSTTSDSSSSSAPRSLNNPFS** VSSSTTSDSSSSSAPRSLNNPFS** VSSSTTSDSSSSSAPRSLNNPFS** VSSSTTSSSSSSAPRSLNNPFS** VSSSTTSSSSSSAPRSLNNPFS** VSSSTTSSSSSSAPRSSLNNPFS** USTSSSSSSAARPSLNNPFS** VSSSTTSSSSSSAARPSLNNPFS** VSSSTTSSSSSSAARPSLNNPFS** VSSSTTSSSSSSAARPSLNNPFS** VSSSTTSSSSSSAARPSLNNPFS** VSSSTTSSSSSSAARPSLNNPFS** VSSSTTSSS							
VIARPSPARPGTWELGRRTEP	1						
SQDPPRGPSGCPWPGRGRGPW RSKTDAAPGKAVARSPAPGASC ELARRGASPGREGLAVGRAAG RGVASG/APSPAEGPGAALGAP PGTHRSSSPSAQVPSSGARTESP W*P*PLLASAGRPRPCPGVHAQE WRKRPRPV*TKRRFPTKAPAR SAGSFETSTFSAHDPGSRGHPW GPKPLPAGGDKTAPFGAQGRGS AJSKAPARHEPETARGHSGSRGG TPGGSSALLCAKNCAPGDPGT AQVQR*SGTQLPPAPLEPLSAP RRVRPVGSGRREKVPRPGRPR RVRPVGSGRREKVPRPGRPR RVRPVGSGRREKVPRPGRPR GPKEATAFNRMKGREGRGSG LLGEGPFKDESNGVSKSK LGEGPFKDESNGVSKSK GEKRRGKAQRWKWPMGGICR QLGVAKSMEGYQSRRDQGGG GVSDKWPQVCAKKPEFYPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPARSMAMHJNPDPFGQ KQNLSPKVADITTDLESSGSGA GKFQVISKSDISEVLLQQMDAG HSSKDPNEYGGWKSPRPRC SAGST SAG	i .		1			1	
RSKTDAAPGKAVARSPAPGASC	1					l .	
ELARGASPGREGLAVGRAG RGVASG/APSPAEGPQAALGAP PGTHRSSSPSAQVPSSGARTESP W*P*P*LLASAGRPRPQGY*PAGE W*RKRPRPVRTKRFPTKAPAA SAGSFETSTSAHDPGSRGHPW GPKPPAGGDRTAPPGAQGRGS ASKAPARHHEPALRGHSGSGGG TPGGSSALLCAKNCAPGDPGT AGVOR*SGTQLPPAPLEPLSAP RRVRPVGGRRREKVPRPGRPR RRVRPVGGRREKVPRPGRPR RVRPVGGRREKVPRPGRPR RSVRRDVEKLEPSDIVCGNVQ CYSCMETNLTVSQKVKHEVTV GPREGATKPNRMKGKEGRGS LLGEGPFFNDESVMSSQGSSKD GEKRRGKAQRWKWPMGGICR QLGVAKSMEGYOSRRDGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPARSNAMHN.PDPPPGQ KQNLSPKVMDIITDIESSSGSGA GKPGVJSKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPC S3546 33914 B 3583 1 503 3547 33915 A 3584 1 787 MIKWVSYQGCRDGLTYGWSCS VETVRWLPEVHAADTSCLKISA CLSSFSSYKARPSVAQAAPPSS PHKTSLCTTSAPISRPSMRTTS APP*USAARPSI*NISSSPESSAA TI*N*NMSSPGLQLHTOTRITS APP*USAARPSI*NISSSPESSAA TI*N*NMSSPGLQLHTOTRITS APP*USAARPSI*NISSGPSSSAA TI*N*SMSSTGLQLHTOTRITS APPFUSAARPSI*NISTSPESSAA TI*N*STSTGSTSHEPPAR TPVPPGSPARTPSGNSHTGSEV VFSSTT*DISGSTGSSHGPPAQR LST*T*AAAPPPGGSISTTIPLIN SGSTTSSSRSSAAPRSI*NINPIS*			1		1	ł	
RGVASG/APSPAEGPOQALGAP PGTHRSSPAQVPSSGARTESP W*P*P*LLASAGRPRPQPGYHAQE W*RKRPRPPVRTKRFPTKAPAR SGSTSTSTSAHDPGSRGHPW GPKPLPAGGDRTAPPGAQGRGS ASKAPARHEPALRGHSGSRGG TPGGSSALLCAKNCAPODPGT AGVGR*SGTQLPPRAPLEPLSAP RV*PYGSGRREK*VPRPGPR RV*PYGSGRREK*VPRPGPR GPKPYGSGRREK*VPRPGPR GPKPGATKPRMKGGGGRSG LGEGOFFKDESVMSSQGSKD GEKRRGKAQRWK*WPMQGICR QLGVAKSMEGYGSRSDGSKD GEKRRGKAQRWK*WPMQGICR QLGVAKSMEGYGSRDGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSVTSCGSYTTTQLCHOL RELEISPARSNAMHLNPDPPGQ KQNLSPKVNDIITDIESSSGSGA GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPPRC GLGVATSVATGATG GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPRC GLGVATSVATGATG GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPRC GLGVATSVATGATG GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPRC GLGVATSVATGATG GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPRC GLGVATSVATGATG GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPRC GLGVATSVATGATG GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPRC GLGVATGATG GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPRC GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPPRC GKFQVISKSDISEVLLQMDAG GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO GKFQVISKSDISTVDPCO G	1		1		1		
PCTHRSSSPSAQVPSSGARTESP					1		
W*P*LLa*SaGR*PRPQGV*HAGE WRKRPRPV*TRRRFPTKAPAR SAGSFETSTFSAHDPGSRGHPW GPKPLPAGGDKTAPPGAQGRGS AJSKAPARIHEPTKAPGRSGGRG AGVGR*SGTQLPPFAPLEPLSAP AJS913 A 3582 1 3339 MSVKRDVEKLEPSIDVCGNVQ CYSCMETNLTVSQVKYHEVTV GPREGATKPNRMKGKEGRSGS LLGEGDF*KDESNMSQGSSKD GEKRGKAQRWKWPMQGICR QLGVAKSMEGYQSRRDQGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSYTSCQSVTITQLCHGL RRLEISPASSNAMHJNPDPPGQ KQNLSPKVMDITTDIESSSGSGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPKPKC A 35914 B 3583 1 503 3546 33914 B 3584 1 787 MIKWVSYQGCRDGLTYGWSCS CLSSFSSYKAPSVVAQAAPPSS PHYSSAARPSI*NISSSPESSAA TI*N*NMSSPGLQLHDTGTRTS APP*USSAARPSI*NISSSPESSAA TI*N*NMSSPGLQLHDTGTRTS APPPVLINSATSGCTTTSAPPRAR TPV*PPGSPARPSPKNSHTTS APPPVLINSATSGCTTTSAPPRAR TPV*PPGSPARPSPKNSHTTSTPLIN SGSTTSSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSSRSSAARPSI*NIPSTPLIN GSSTT*SSTSSRSSAARPSI*NIPSTPLIN GSSTT*SSTSSRSSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSSRSSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSSRSAARPSI*NIPSTPLIN GSSTT*SSTSTSSTSTSTSTSTSTSTSTSTSTSTSTSTST			1				
WKR.RRR.PVRTKR.FPTKA.PÅR SAGSFETSTSAHDPGSRGHPW GPKPLPAGGDKTA.PPGAGGRGS ASKAPAR.HEPALR.GHSGSRG TPGGSSALLCAKNCAFGDPGT AGVGR*SGTQL.PPA.PLEPLS.AP RRYKPYGSGRREKYPRFGRPR RRYKPYGSGRREKYPRFGRPR RRYKPYGSGRREKYPRFGRPR RRYKPYGSGRREKYPRFGRPR GPKPGATKPRIMKGKGKGRSG GLGGDFFKDESVMSSQGSSKD GEKRRGKARW.WPMGGICR QLGVAKSMEGYGSRRDGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSYTSCGSYTTTQLCHGL RRLEISPARSNAMHLNPDPPGQ KQNLSPKYNDIITDIESSSGSG GKFQVISKDISEVLLQMDAG HSSKDDPNEYGGWKSPRPKC A 33915 A 3584 787 MIKWYSYQGCRGLTYGWSCS VETVRWLPEVHAADTSCLKISA CLSSFSSYKAPSVVAQAAPPSS PHKTSSLCTTSAPSRPSMRTTS APP*SSAARPSI*NISSSPESSAA TI*N*NMSSPGLQLHOTIGITS APPFVLNSATSGITTSAPPRRR TPVPPGSPARTPSGNSHTIGSYC VFSSTT*DIGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTTPDLN SGSTTSSSRSSAPRPSLNIPFS*V GSTTSSSRSSAPRFSLNIPFS*V SGSTTSSSRSSAPRSLNIPFS*V GPKPGSPALTPSGNSTITSPLNIPFS*V GPKPGSPALTPSGSSTTPDLN SGSTTSSSRSSAPRSLNIPFS*V GFTSTSSRSSSAPRFSLNIPFS*V GPKPGSPALTPSGSSTTPDLN GSGTTSSSSSSAPRFSLNIPFS*V GFTSTSSSRSSAPRFSLNIPFS*V GFTSTSSTSSSSAPRFSLNIPFS*V GFTSTSSTSSSAPRFSLNIPFS*V GFTSTSSTSSSSAPRFSLNIPFS*V GFT			1			ł	
SAGSFETSTENAHDPGSRGHPW			1				
GPKPLPAGDRTAPPGAQGRG			1				
AISKAPARJHEPALRGHSGSRGG TPGISSALLCAKNCAPGDPGT AGVGR*SGTQLPRAPLEPLSAP RRVRPVGSGRRREKVPRPGRPR RRVRPVGSGRRREKVPRPGRPR RRVRPVGSGRRREKVPRPGRPR RRVRPVGSGRRREKVPRPGRPR RRVRPVGSGRRREKVPRPGRPR RRVRPVGSGRRREKVPRPGRPR RRVRPVGSGRRREKVPRVGRPGRPG RRVRPVGSCRRESDIVCGNVQ CYSCMETNLTVSQKVRHEVTV GPREGATKPNRMKGKEGRSGS LLGEGPFKDESVMSSGGSSG GUSDKWPDVCAKKPEFVPTAQ VWANFSVTSCQSVTITQLCHGL RRLEISPARSMAMHLNPDPPGQ KQNLSPKVNDIITDIESSGSGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPC STANFART			1				
TPG/GSSALLCAKNCAPODPCT			1				
AGVGR*SGTQLPPRAPLEPLSAP AGVGR*SGTQLPRAPLEPLSAP 3545 339913 A 3582 1 3339 MSVRKDVEKLEPSDIVCGNVQ CYSCMETNLTVSQKVKHEVTV GPREGATREPNRMKGEGGRSGS LLGEGDFFKDESVMSSQGSSKD GEKRRGKAQRWKWPMQGICR QLGVAKSMECYQSRRDQGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSVTSCQSYTITQLCHQL RRLEISPARSNAMHLNPDPPGQ KQNLSPKVMDIITDIESSGSGA GKFQVISKDISEVLLQMDAG HSSKDDPNEYGGWKSPRPRC 33915 A 3584 1 787 MIKWVSYQGCRDGLTYGWSCS VETVRWLPEVHAADTSCLKISA CLSSFSSYKAPSVAQAAPPSS PHKTSSLCTTSAPSRPSMRTTS APP*SSAARPSI*NISSSPESSAA TI*N*NMSSSPGLQLHDTGTRTS APPRVLNSATSQTTTSAPPRAR TPVPPGSPARRPSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTTYDLN SGSTTSSSRSSAPRPSLNNPFS*	į.	į .					
RRVRPVGGGRREKVPRPGRPR		l	1				TPG\GSSALLCAKNCAPGDPGT
			1				
CYSCMETNLTVSQKVRHEVTV							
GPREGATKPNEMKGKEGRSGS	3545	33913	Α	3582	1	3339	
LLGEGDFFKDESVMSSQGSSKD GEKRRGKAQRWKWPMQGICR GEKRRGKAQRWKWPMQGICR QLGVAKSMEGYQSRRDQGGR GVSDKWPQVCAKKPEFYPTAQ VWANFSVTSCQSYTITQLCHGL RRLEISPARSNAMHLNPDPPGQ KQNLSPKVNDIITDIESSSGSGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPRC GKFQVISKDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPRC S33915 A 3584 1 787 MIKWVSYQGCRDGLTYGWSCS VETVRWLPEVHAADTSCLKISA CLSSFSSYKAPSVAQAAPPSS PHKTSSLCTTSAPSKPSMRTTS APP*SSAARPSI*NISSSPESSAA TI*N*NMSSSPGLQLHDTGIRTS APPRVLNSATSQITTSAPPRAR TPVPPGSPARPSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTTYDLN SGSTTSVSSRSSAPRPSLNNPFS*		1	1				
GEKRRGKAQRWKWPMGGICR QLGVAKSMEGYQSRRDQGGR QVSDKWPQVCAKKPEFYPTAQ VWANFSYTSCQSYTITQLCHGL RRLEISPARSNAMHLNPDPFQ KQNLSPKYNDIITDIESSSGSGA GKPQVJSKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPRPC 3546 33914 B 3583 1 503 3547 33915 A 3584 1 787 MIKWYSYQGCRGGLTYGWSCS VETYRWLPEVHAADTSCLKISA CLSFSSSYKAPSVAQAAPPSS PHKTSLCTTSAPISRPSMRTTS APPINASSPGICLHOTGTRTS APPINASTSGICLHOTGTRTS APPRVLINSATSGICTTSAPPRAR TPVPPGSPARTPSGNSHTGSEV VFSSTT*DISGSTGSSHGPPAQR LS*T*RAAPAPPGGSISTTIPDLN SGSTTSSSSSKSAPPSLNNPES*							
QLGVAKSMECYQSRRDQGGR QVSDKWPQVCAKKPEFYPTAQ							
GVSDKWPQVCAKKPEFYPTAQ					1		
VWANFSVTSCQSVTITQLCHGL RRLEISPARSNAMHLNPDPPGQ KQNLSPKVNDIITDIESSSGSGA GKFQVISKSDISEVLLQQMDAG HSSKDDPNEYGGWKSPKPRC	1		1				
RRLEISPARSNAMHLNPDPPGQ KQNLSPKYNDIITDIESSSGSGA GKFQVISKSDISEVLLQMDAG HSSKDDPNEYGGWKSPRPRC			1				
RQNLSPKVMDIITDIESSSGSGA	1		1				
GKFQVISKSDISEVLLQQMDAG			1				
HSSKDDPNEYGGWKSPRPRC			1				
3546 33914 B 3583 1 503							
3547 33915 A 3584 I 787 MIKWYSYQGCRDGLTYGWSCS VETVRWLPEVHAADTSCLKISA CLSSFSSSYKAPSVVAQAAPPSS PHKTSSLCTTSAPSRFSMRTTS APPYSSAARPSI*NISSSPESSAA TI*N*NMSSSPGLQLHDTQTRTS APPRVLNSATSQTTTSAPPRAR TPVPPGSPARPSQKNSHTGSFY VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTTPDLN SGSTTSSSRSSAPRSLNNPFS*			_				HSSKDDPNEYGGWKSPRPRC
VETVRWLPEVHAADTSCLKISA CLSSFSSSYKAPSVV VAQAPPSS PHKTSSLCTTSAPSRPSMRTTS APP*SSAARPSI*NISS/SPESSAA TI*N*NIMSSSPGLQ.HDTOTRTS APPRVLINSAT/SQTTTSAPPARA TPVPPGSPAPRSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTT\PDLN SGSTTS/SSRSSAPRPSLNNPFS*							
CLSSFSSYKAPSVVAQAAPPSS PHKTSSLCTTSAPISRPSMRTTS APP*SSAARPS!*NISSISPESSAA TI**N*NMSSSPGLQ.HDTQTRTS APPRVLNSAT/SQTTTSAPPRAR TPVPPGSPAPRSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTT\PDLN SGSTTSJSSRSSAPRSLNNPFS'	3547	33915	A	3584	1	787	
PHKTSSLCTTSAPSRPSMRTTS APP*VSSAARPSI*NISSSPESSAA TI**N*NMSSSPGLQLHDTQTRTS APPRVLNSATSQTTTSAPPRAR TPVPPGSPARPSGNSHTGSEV VFSSTT*DISGSTGSSHGPPAQR LSTT*AAPAPPQGSISTTPDLN SGSTTSSSRSSAPRSLNMPFS*			1				
APP*SSAARPSI*NISS/SPESSAA TI*N*NMSSSPGLQ.HDTQTRTS APPRVLNSAT/SQTTTSAPPRAR TPVPPGSPAPRSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTT/PDLN SGSTTS/SSRSSAPRPSLNNPFS*			1				
TI*N*NMSSSPGLQLHDTQTRTS APPRVLNSATSQTITSAPPRAR TPVPPGSPAPRSPGKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTT\PDLN SGSTTSJSSRSSAPRSLN\PFS*			1				
APPRVLNSAT/SQTTTSAPPRAR TPVPPGSPARPSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTTPPID.N SGSTTS/SSRSSAPRSLNNPFS*			1				
TPVPPGSPAPRPSQKNSHTGSFV VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTT*PDLN SGSTTS/SSRSSAPRPSLNNPFS*	1		1				
VFSSTT*DISGSTGSSHGPPAQR LS*T*KAAPAPPQGSISTTNPDLN SGSTTSSSRSSAPR*SLNNPFS*	1		1				APPRVLNSAT/SQTTTSAPPRAR
LS*T*KAAPAPPQGSISTT\PDLN SGSTTS/SSRSSAPRPSLNNPFS*			1		1		TPVPPGSPAPRPSQKNSHTGSFV
SGSTTS/SSRSSAPRPSLNNPFS*			1				VFSSTT*DISGSTGSSHGPPAQR
			1				LS*T*KAAPAPPQGSISTT\PDLN
NSAVKKSAAEVNE	1		1				SGSTTS/SSRSSAPRPSLNNPFS*
	1						NSAVKKSAAEVNE

SEQ ID	SEQ ID NO:	Mct	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3548	33916	Α	3585	746	2018	THPQERGTWGNRQLFAVLPLPF
		1				YTSLETMSMGCGAVVAGQYQ
						KCPFFTIPSANFPWQKQEGMSG
						NPPRVRRHISLSRSCLTLAVPMT
					I	IRRSWEGAPFVGAQDGCRPLLP
					•	GRRALLLHLGLAPLL/GPPPPPV
						SPPWPPCKATWVSAGGRCLY/G
	ļ					CPSAPAPR\APPEFPAPPGFPAPP
						AASSPSTRCSRGT*SCGPGRPGP
				i		LGPAWSA\GQRGQLAVPEPLQA
						VLGALGLLRPLGERR/PAQAGT
						FSPTAPGRGAPGASA*GGRISG
						HSSGDIPRRGPSRGHPPLLAQGS
						DAIRSTLI-I/ERLSTRTRPSFKIKT
					i	PSPHQRPQQPHASWTPSSGTLS
						KPSTPCSSSSCAPRSGDGGG/EG
						HAGLPSOPAAGSOPAAPCORPE
						AWAGGRGNRPGKPGAPQGPCF
						SLPRPORSR*LPPPAROKPPFFTL
		l				LSLFSF
3549	33917	A	3586	1	1911	TIYAVNLFPILPQGDL*PFTMVT
						MHWGEGNGQIFRGLLDTGSEL
		ŀ		l		MLIPGDPKCHCGPPVKVGAYES
				l		QVINGVLAQVQLTVVPEGPQT
		ŀ		l	ŀ	HPVVISPVLECIIGIDILGSWQNP
				l	[HVGSLTGKVRATMVEKAKWK
						PLEQPLPRKIVSQQQYRIRGEIA
						EISAKIKDLKYAGVVIPTTSPFK
						SPIWPVQKTDGSTKIPGTSTSVK
		1			ļ	FLGVQ*CGTCQDIPSKVKDKLL
				1		HLAPPTIKKEAQRLVGLFGFWS
			i	l		QHIPHLGELLRPIYRVTRKAASF
						EWGPEHEKALQQVQAALQAAL
						PLGPYDPA/DQATVQLKLPVIN
		1		Ì		WVL\SDPSSHKVVMHKLREEV
		1				GQMTMVFTPATLSSLPQHAMM
						VSWGVSYDQLTEEEKTRAWLT
	İ		l			DRSARYAGTTRKWWTP/HQSLS
			l			PATPVI/SQWA/HGHGGRGGGY
		1				AWAQQHGLALINADLATASAE
						CPICQQQRPKMSTRYGTIP\GKV
						LQKAVCDLNQHPIYGTLS/PIAR
						IHRSRNQGVEVEVAALTITPSDP
			Ì			LAKFLLPVPTTLRSTGLEVLVPE
						GGKLPPGDTTTIPLNRKSRLPPG
						HFGPLLPLSQQAKKGVYPPKKK
						SLYQKHALSYMSLFTAVPFTIA
						KTWNQPRFPSMVNWIENMWYI
			1			YTMEHYTAIKMSEIESFAAIWM
				l		QLEAI
3550	33918	С	3587	44	310	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3551	33919	С	3588	20	328	
3552	33920	С	3589	288	542	
3553	33921	Α	3590	332	528	
3555	33922	A	3591	3	191	NVCQSHRIPEHCVDSLNVCSS* GIPEYSCCDLNICPSHVTPEHCY EGLNDCPSSNIPEHCCWGLNDC SSRSIPOHCFWGLHVCPLHRIPE HCSWVLSVPSQRILEHCDENL VCL*HRIPEHSRCCLNVCPSHE IPEHCCLESESLSLTODSRTLLL **USSECLSET**NSILPPLFECLS* T*YSKTLHLGSECLSLT**DSRTS LLWSECSSYDVENTTA*EGLSI T*YSKTLHLGSECLSLT**DSRTS LLWSECSSYDVENTTA*EGLSI T*YSKTLHLGSECLSLT**DSRTS LLWSECSSYDVENTTA*EGLSI T*YSKTLHLGSECLSLT**DSRTS LLWSECSSYDVENTLA*EGLS ECTSHRVPEHCYEGLNCPSRRIPEHCYE GLHVRFSRGIPEHSCCRLNVCPSR HRIPEYYYECLNICPSKRIPEYC CLVPSYYSSHRIPEHCY**ULNDE HRYEGLNVCLSHRIPEHCYEGL YDCPSHRIPEHSCEGLKVCPSHI IGEYCCWLSVCPSHRIPEHCY HCLNVCPSHRIPEH**EDSRTLLL SECPSQRISEHCYEGLNVPPSH RIPEHCYEGLNDSPTHRIPEHCY EFLNDCHSHRIAEHCFSGLNLC LSHRILEHREWGLHVCPSHGLE HCCWDLSVSHSH/SNSRSL**RVS
		A				
3556 3557	33924 33925	A	3593 3594	19	367	AIQSWCHHVLQAQPHVELLVP RFIEELGSLVHGH*PRHRLPPAH SHVLHHCQLQLGHTLRPRHCIL QEHACG/RVRCLLQRQAGSPGG WCKRECLFLQE/VKPSVRICTVE MCTISIS
3558	33926	A	3595	55	555	NHFVAEAASCPPRCPFRLDAKK LVRSPSGLRMVPEHRAFGSFD LEEPGWVPDKECRRCMQCDAK FDFLTRKHHCRRCGKCFCDRCC SQKVPLRRMCFVGPRAAVRGS APWVFPQGGGVFTD\NSSKCS* AEPPSSXQFGNSEKPETMT/VSS FQ*PEILVSGWRQPL

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (N=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3559	33927	A	3596	182	696	PVFWIRNL*SMASRGLRRD*EH LKEAILAHSL/KAKRGGEAAEE ESEASRGWLVRFKGRRCLRNIE VQGETASAAGEAAAGHPGDLA KITGAGGYYTQQIFSVDETTLH WKKMPCRTFTATEEKISAYFKA
3560	33928	A	3597	74	2521	SKDGLNLLLGVNAPGTYVLRS NISVFLSEEMSSDKRLTEMGY RERWAAGPVTCQVTTWPGAAT TRVTWPMTRPATPCAVHGCSC PRSHWSOKCGOPASRAV/SPHP
						PSTCGSSA/APGPTPKQEAPSAL WPLSGFPN*EPGPGQPGD\VVE KATERMAAMKTEAGVPLVEV QDPVEVPSGR/PAGTCPAQPQH RTPAPCTADP/PALDTPTTTHPA PAPCPTAIAASWPAVWLPQPG
						Q*PRCPRLIATCEGQTPAGEEPQ AAATAGEGR/VKASVSPAPRGT PCCGIRWVARPAFSGHRSSPCP GSQGCWA/PSSGVPEASEPRPGE QEPIFRKREFNKEIKSL/PEPAGV PRPAWLLSAP*APSHAELPG*PP
						PLPCPAKRGPPGCG*APWRPLP RRPSSV/PPPAWSPP/QDLPPLGS EPAKPTNGG/PALCFPPPHSLQP QDASEKTQG/PEEAPPPCLVPR WPPDSNSR*HPRRSPMSPAPHS
						TPGRRHLTQIPNYKTHLFP*APA RGPSPGRACTSPCPRQGLWWR WPAARATSGALSHLHFPPTPA LPATFSLSSLQLPLHLPPHCVQR APAAAAGSRRRSRCPPSRRSPA
						CLTSPTAFMRSSPTS*PSRQPPW SSASTSSKRTSVSSWASSPSPSP TCSGTFPWA*RR*KAPASTCPR RPTGAACCVNWRSPKGPGRPP
3561	33929	В	3598	1	588	GSAPPTAAQRHPLCSRNQPPTL PRTRPQSPAAPSTPTCQPAGSSA LWSPSSTCLPAPAWVPVPPSPR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
		_				
3562	33930	Α	3599	357	1011	FLPLGELYAEGSRMIWSDGFW
		1				AGHLHSCSHPRSSSFSPTCTYPL
		l				PPPPPWVERQGTRGSG\P*PGKR
		1			I	TSSPFRVSPGSNTRECTPS\GLLD
						CIPSCISLSEKPQNDSSSESA*KIP
					1	ASSLVTSGLGFCKNPQWSNTSC
						TSLSCDA/CPPWND/CCQMPVPC
	i	l				SWTFQPPEP*AK*TSVPYKLPSL
		1				WYSVSQRGKDSPSPAPPGPGRR
i					ŀ	AQPASRAAAAPPAVGP/SDRAA
l		1				DPLSPLQAPIWAPRHQHGRSPR/
l		ŀ				VR*GLRWLHGALRVVVILEGG
		ŀ	i			RAQ*PPWNDFVRCQCHALGLSS
1	l .	ŀ				LQNHEPNKLLFLINYPVCGILCP
l		ŀ				NAGKTARAPPLRARVGAPSLPA
	i	1				ALLLLLLWDR
3563	33931	Α	3600	63	660	KPQVNKSASCAQLAGPVSQRG
						KDSPSPAPPGPGRR/CPACQPRC
		ŀ		i		CCSSCCGTADRAAAPLSPLQAPI
ŀ		ŀ	1			WAPATSMDARRVPVRVFALTE
ĺ		1				ART*GRAPWAFPGDVNPSLAPI
				1		P*TCSYTELIPPVSFSFPPSTSGN
						SPTACLDSGVQLASPSGSRTGA
ŀ			į.	1		TGGAAHSPARAPA/PPQPLGSR
						WDQGLR WLHGALR VVVILEGG
ł				l		RAQ
3564	33932	Α	3601	202	515	FCKHEAAVSSGKAVGTRSQCR
						HSGPLRVAMKFPARSTRGATN
						KKAESRQPSENSVTDSNSDSED
						ESGMNFLEKRALNIKQNKAML:
						AKLMSELESFPGSFRGR*PRGCS
l	1	1	l			AAPRSKRRSGHPPPAWT/CSPR
l			l			AAERS/PE*RRT*RNSDM*S*FP
		l			i	ARSTRGATNKKAESRQPSENSV
	İ					TDSNSDSEDESGMNFLEKRALN
	1	l				IKQNKAMLAKLMSELESFPGSF
			1			RGRHP
3565	33933	С	3602	40	186	
3566	33934	Α	3603	1	3189	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3567	33935	Α	3604	I	1821	MLKNFKKGFNGDYGVTMTPG
					\	KLRTLCEIDWPTLEVGWPSEGS
		1	l			LDRSLVSKVWHKVTGKSGHSD
		1				QFPYIDTWLPQWVRGQAAAVL
ŀ		1				VAKGQIVKEGSRSTHRGKSTPE
		l	l		1	VLFDPTSDDPLQEMAKVIPVVP
İ						SPYQGERLPTFESTVLVPPQDK
1						HIPRPPRVDKRGGEASGETPPL
		1				AARLRPKTGIQMPLREQRYTGI
						DEDGHMAERRVFVCQPFTSAD
						LLNWKNNTPSCTEKPQALIDLL
	1					QTIIQTHNPTWADCHQLLMFLF
	i					NTDERRRVLQAATKWLGEHAP
	I					ADYQNPQEYGKEESPAQFYER
						LCEAYHMYTPFDPDSPENQRMI
ľ						NMALVSQSAEDIRRKLQKQAG
	1					FAGMNTSQLLEIANQVFVNRD
	İ			'		AVSHTGAEHSVVTGPVAPLSK
	i					KTIDIIGAMGVSAKQAFCLPRT
ŀ						CTPGTKDYRLVQDLRLVNQAT
	İ					VTLHPTVPNPYILLGLLPAEDS
						WFTCLDLKDAFFSIRLAPERQK
						LFAFQWEDPESGVTTQYTWTW
1						LPQGFKNSPTIFGEALARDLQK
						FPTRDLGCVLLQYVDDLLLGHF
	ŀ					TAVGCAKRTDALLRHLEDCGY
						KVSKKK\AQICQQVRYLGFTI
						RRGV\RLGSERKQVICNLPEPKT
3568	33936	Α	3605	1269	2463	GVQEESSDLPTAVDSSRPDIRD
		1				QAWASVHWELYVHGSSFINT*
	ŀ	1				GERGAGY/AVITWT/HVVEARS
İ	ŀ	1				MPQGTSAQKAELIAFIRALELSE
	1	l		1		ALAKTVRQRCVSCRQHHARQG
	i	l		1		PAVPPGIQAYGA APFEDLQVDF
					ľ	TEMPKCGDIRKIVTGDVNTPAI
				1		LGVVSSSPPSHIGNNITEDPELQ
		l				PILAGLSLSMYLVTVLRNLLIIL
						AVSSDPHLHTPMCFFLSNLCWA
		1				DIGFTLATVPKMIVDMQSHTRV
1						ISYEGCLTRISFLVLFACIEDML
1	1		l	1		LTVMAYDCFVAICRPLHYPVIV
1	1			1		NPHLCVFFLLVYFFLSLLDSQL
1	1	1	l	I		HSWIVLQFTIIKNVEISNFVCDP
		l	[SQLLKLACSDSVINSIFMYFHST
				[MFGFLPISGILLSYYKIVPSILRIS
2560	22027	D	2606		1020	SSDGKYKAFSTCGSHLAVVC
3569 3570	33937 3393 8	B B	3606 3607	I	1830 459	
3571	33938	В	3608	30	440	
3572	33940	A	3609	1	279	
3573	33941	A	3610	2	500	
2213	JJJ941	<u></u>	2010	14	500	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide sequence	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3574	33942	A	3611	370	464	GHACGAERDHLQPHSPAHLLL LLLSV*AVW*PRYTVKMATAC HQW
3575	33943	В	3612	1	780	
3576	33944	В	3613	1	610	
3577	33945	Α	3614	1	1896	
3578	33946	Α	3615	2	1418	
3579	33947	A	3616	314	720	GVQEESSDLFTAVDSSRPDIRD QAWASVHWELYVHGSSFINT* GERGAGY/AVITWT/HVVEARS MPQGTSAQKAELIAFIRALELSE ALAKTVRQRCVSCRQHHARQG PAVPPGIQAYGAAPFEDLQVDF TEMPKCG
3580	33948	A	3617	1	1029	
3581	33949	A	3618	1199	1758	KTLSFLSDQPLRARSCLPFSGKI RS/RALAKTVRQRCVSCRQHHA RQQPAVPPGIQAYGAAAFEDLQ VDFTEMPECGGNKYLPVLGRT YSGWVETYPTRAEKAREVTRV LLRDLIPRLELPFRIGSDNGPAF VADLLQKTATVLGITRKLHAAS RPQSSGKGIQNNRTGGVYTPCD IESHVILFRSGY
3582	33950	С	3619	499	831	
3583	33951	A	3620	410	1144	LSIQQYLTRP/PLLGFPPAEDSW FTCLDLKDAFFPIRLAPERQLLF AFQWEDPESGWPPCWRALAAT ALLVOGANKLTLGOKLNIKASR AVVTLMNTKGHHWLTNATLT DYQTLLCENPRITIEVCNTLHPA TLLPVSKSPVKPGCVEVLDSIDS SRPDLWDQPWASVDWELYLD GSSPFLQPPRRGGGYA/VGDTSE LPPCWVCGIPALTQRLEKQHLP PSGHQGSLKHLIWDLLLLTKKR TFSSMI
3584	33952	Α	3621	1244	2690	
3585	33953	В	3622	1	1114	
3586	33954	В	3623	1	1863	

SEQ ID	SEQ ID NO	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	-			sequence		
3587	33955	IA	3624	13	2056	REALOGIOVELKHLETFGIJVPC
2007	50700	1		[OSPCNTLLLPFPKPRTKDYSOV
		ı				QDLRLLHQATLTFHPTVPNPTT
		1				LLGLLPAKDSGFTCLDPKDAFF
		1				PIRLAPEROKLFAFQWEDPESG
		1				VTTQYTWTGLPQGFKNSPTIFG
						EAWARDLOKFPSRDLGCVLLO
		1				*VDDLLLGHPTAVGCAKGTDA
		1				LHRHLEDCGCKVSKKKAOICR
		i				QQALAATALRVQEANKLTLEQ
1		ŀ				NLNIKASRAVVTLMNTKGHHW
		ŀ				LTNARLTQYQTWLCENPRITIE
١.		ŀ				VCNSLHPATLLPVSESPVEPRC
		ı		i		VEVLDTIDSSRPDLRGOPWASV
						DWELYVDGSSFFNPQGERGAG
					l	CAVITLDTVVEARSLSQATSAO
		1	1			KAELIAFIRALELS/EGRKGLSPC
i		1				RGKDK*WRKDGFGYRMGEYC
l l		1		1		ATAARSCSCTGCARNHPSTSGV
1		1		1		TGKVVRPVFLHLAFVS\FAKTV
				i		RQRCVTCRQHDARQGPAVLPG
				1		GAYGAAPFEGLQVDFTEMPKC
			ĺ	1		GGNKYVLVLVCTYSGWVEAYI
				i		TLTEKAREVTRVLLRDLIPRFRF
				į		PLRIGSDKGPAFLAALLQKTAK
				1		MGTRSDTQLAHIGTVLRDIHVS
		1		1		VCSDGPNLRTGLNVILGGVEW
						QSTPGNLVRRQGETGLHLHIYH
		}		Į.		WWQAVAIFPVYLGSSLHMKVG
	1			1		GRSFEQEEDTEHIPVSYDREGQ
						ECDTELKGQEGDELEAGSVVP
3588	33956	Α	3625	491	964	RIQLCCRTRGTGAQKKRMKVS
	1			1		SRCTPAPATRGTGAWQPQAQQ
				1		APGVRATEAPRL*AHDEVSQPA
	1			1		PAPPSTRHSPRR*PVAGKEHLE
	1			1		AAVDKERHEVAQAVVTHVLEC
	ľ			1		QLEDVAPAHAAQI/GSPPWAGK
	İ			1		RLRTNPAPRPCHPIQTLSRRLGP
		 		ļ		QNHTLLH
3589	33957	Α	3626	131	351	NVGLKGTAGER\GGSGPPS*PPA
						GRNSGPAGRRPPAARAPTPGSA
						AR*PAPPGPPRPPAGRGAAAAA
	22050	+-	2 (28	ļ	100	GPAGGGA
3590	33958	Α	3627	3	428	GEWEAPPLLRHTRPGPA/PAPPA
						PSGASCAPCGGQTCRPRPLRQA
						PPSPITTGHARIWLGQPRPRSSS
	1	1				ATPPKELP*GPTE\PHTGELWVA
1	1	1				SGSCPSGTKLPEEGSGSNTYFSA
		1				VSAGDTQSNIIWNGPPANSNRP
	L			1	L	AAEGPDC

*=Stop coden, /=possible nucleotide deletion, \=possible nucleotide insertion)
deletion, \=possible nucleotide insertion)
YLASAAIFRNMSSVVCLVCFFF
TSQICLQTDNAPYTVLSINENLS
VLGSMFSNFLRSFLRSTKASAK
PFIVTLLRSSFFSVSSSLASSSAM
HSCSSSNSSSFFNSSRTTSKSSST
SSSFTPS/SESF/SS*VSSSRFHSYT
PW
LPAGFGPCGAWNONOREKRPO
SPGAESAA*SGGGQQRGGRAG
AGGHGACASLGSE/PQGREPAL
GAGGETALPSGSGSGRPPRPOR
PRDSGPEALPSAAFWKRRR*AS
ASAPALTPVPDSVRGAQPGGG
GAEPEGKAVRMRGASRPALSQ
LSGREIGPCPQGRVVAPSGTAC
PMVWSCASAARLPEPGNGALL
RTSSPRCSP/CPSAA*LTRLPPT/P
/PGDPSAAPSPGQRPAGLAGAG
GAERSGAVEVGPREPGRDGAG
S*SWI/AGPPGRLEAGSA/GVLR
SPVAGWRPGTCAGRP/GKAGDL
GPSAPPQAPHPPPPSWSPLSPLA
SPPTK
LATTARCEURORATURE ACUITA
LALTARSSHPQRATVPKASVVA
AASPTKFRHSGAALQWRNLGP
VRAQGRRLSTAAPAAPSRRLFP
PPPFRGGRGGGWSGSRGRRGA
EPGRSHGAGGPGDDGRCGWGE
GAGTSTPARPSRGPG*RPEIWTR
GGGGSAKSQG/PAGAPGCAGPR
GASSFGRQRAPAVLGPG/SSTA
VCPLPRRTWNLRAPGGAPSYA
QVAAAHQAPPGRPPWSPRGAR
GSGRSRTFAPSTPAVVAGAASA
VAPPRLRPSPPPAPAPAAAATA
AERRGREEAPGRGCGSGRAEPP
PLGPDGTQVSPLQRSSRVTEFC
GGSGGHYARFWHSSPLRVGAS
RSQS
HGLVLDVRGPLSHAAPYWAPY
PAATAAAARTAPLPPRSAIV*/S
GPQPDFQELRKTWPSQC/GMAR
REPLLPITAIPRVVVETTP*GFA
KQEPSVAGLRCRGSEAPA*LLH
GVHRNVS/ETPGPEMGRPG*GN
HRQRPGKQRGIPSSGLPGRCSG
SRGPHSSPGQKPHGSTLSGRRG
ADPRPRRRVYLSTPLLCEKKPH
HDTILKRKPGMGDGNNPCPWN
AGLYGQATRFAPLPLCPRRRHG

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3597	33965	А	3634	2	339	WPCGWTGRGGCRQ\RGRERRL GSGVRFGDVSFRGRGRGRARA SWKPPHQGPGEPKSGTRNRPP*\
						GGGAPAGIRGPELGTGNMKKL LLSLPIYYHLAGEKGQVAKIVRI PSADV
3598	33966	A	3635	31	438	MYTDVYTRGGELGQRHYPPGE SSGLFCGQCGERETRDPSYRG WSRFRFRALKNGAHWSPRLA VFGDLGADNPKAVPRLRRDTQ QGMYDAVLHYGNFSNYKARF SMPGDNEGLWYSWDLGPAHIIS FSTEVHFFLH
3599	33967	Α	3636	I	422	LRRDTQQGMYDAVLHVGDFA YNLDQDNARVGDRFMRLIEPV AASLPYMTCPGNHEERYNFSN YKARFSMPGDNEGLWYSWDM GPAHIISFSTEVYFFLHYGRHLV QRQFRWLESDLQ/QSQ*EPGSP AVDHHYGAPAHVLTK
3600	33968	Α	3640	I	319	FRREPPRGAAAAAALPRRNREN KRSKNRPCCEGPRGSARMKELE *PRPLQVLCLLPEMCSPRLADS *YSPVSVRPISAPVRFLHRCCPPP FAEFPACRLLQHSRVPL
3601	33969	С	3641	214	363	
3602	33970	Λ	3642	1	3390	
3603	33971	А	3643	396	766	ERGLGRSEIPRKEVEHFMQLGS AVAGP*LLPLVGPAGECFHGW LEPLLARIAEDKTVVVSPDIVTI DLNTTEFAKPVQRGRVHSRONF DWSLTFGWETLPPHEKQRRKD ETYPIKQPVGVIGD
3604	33972	A	3644	105	786	VGPEHCAGAARWYTSPPRSWP DAGGSVNP DLP*REKHPEG(G* KLQGQGAKTAGNAVVWKPLS K/PQGSSALSGGHWDRLPAPDP GKMPNCDRAPPKIASRVSPQAC FPRSPPVPSAGPLRASTPADQA RRPARAARPPDALSKRGPCRIS AKLHSGGGGGGGCREKAQEEP EGRTARSLTPPLPLAPRPGPAGR RLPPAHTTQPPGRTGCPSPAGR DTSQLPYFLLK
3605	33973	A	3645	313	546	RNKVGSRGRAKQLKFSGQSTR VHRSESREEEEEKEEDEEEEEE EEEYEKEEEKEEEEEEERDLEF SKGPFLSS*SSQGK/GTRVHRSE SREEEEKEEDEEEEEEEEEEE KEEEKEEEEEEERDLEFSKGPF

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide sequence	hod	in USSN 09/540,217	location of first codon for peptide	eodon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/340,217	sequence	or peption sequence	deterior, (-possione nucleoride insertion)
3606	33974	A	3646	3	1332	PLGPRRQQSECGAPTLTWPPGS
2000	337	l.,	2010	ľ		NGLPGOOGASPLSASPGAGAGS
						GRGPAA\GGSGASCTPSPRGPAS
		1				WSRSAAQVPRSSRWRAGSASS*
		1				NAGSP/TPPTSQPPRA/PALCAA
		1				AGTLAPVEKGVEVPAGRGLSG
		l				APS**GKCPLPEAPSGGSAPLS*
						GGTESGAGAPEPRKATGRPGPR
						VPGGAGAA/RGLPAPTSGCAAP
						FPPRPCPGLCVLRARPAGAAHP
l						CPGPGWPG/PGPGAHQTLRAAL
1						REPSPLASPLVSGRPGPRLVFNR
						VNG/AAGPLHVPILRGDPGDLH
		l				SGPRGECPLCVRSLAAGATAA\
		١				DGGPAGEGRPRPVYTMERTAN
						PRLQNFVPH*PR/PSGGRKQFLA
		ł				RITS\FPSGCWEGGAATRPTCRQ
1						EKGMAALPTHCAWLGAGHT*K
	Į.					CQHLDFCTFFFPGPGCGDGRCH
ŀ	ĺ			1		VQGPNPSDLSPAHCAQGPATSP
						WGWQGGAPG
3607	33975	Α	3647	102	788	GHCGGGTQCSWPAPWCQNLLP
l						PSASPTLSTQRQLWHAWPGAH
			1			RNPV*QVPSLDS*ARAQLSVPA
						QGSLPLC/ASLTASPWCSCSSLA
		1				VLLFGK*PFCVNLF*RASLMKS
	ļ					SSRARVLPSLRPVRWPAVG\RG
						WQGMERGQGAWPWLCGAVCS
		1		ĺ		RA*SVHMTTLPSGPALCGIQRR LQSSTQRRPESLHPLQLGWEAA
	ł					QAGEGLPHPAVVHLPASPRLQL
						SQLHQSRPRLPPG
3608	33976	A	3648	114	1309	TNCSCLRDRPLDSSHVPWVEEA
3000	33370	ľ`	2040		1307	QSAHNNKEIVPQKGPWSSKHN
	}	l			İ	QARGPPRSESNTNKAVNCAGRS
l	ì	l				TKTQTPRGTSGT/TEGNT*VHTR
	1					HTKMSTTNTNTSSLDAPPTTQQ
		1				MRSTRERGTS\PAPPSSALKNTY
		1		ļ		TLPLPTS\SNDTTIYQLTVVPGP
		1				GPRTGELPRCHARVTPRVSGEE
	İ					ALPPPPRSPENSNTHLRTPSQTR
						TPTRARPPL\PETSPQQPWPDPR
ŀ		l				VGFFLRSSPVWAPSSQQYPWW
	1	1				SPSLSTNMTIPPESS/SLLPTLAY
l	l		1			YTSLTSHHGQRMPA/PADHA*A
	1		ŀ			QSTPSAHRHRPQYVQWTTDPPS
				l		THGTFEESSGR/YPQTHTVAVK
					l .	KKTIGTPARDSHSFPTTPTTRM
						VKSLKTSTGTSTDLSSSRSILKS
			1			PTSSIFTSLTIFSIWRDPDSMDLC
	i i		1			V

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	or peptide sequence	deletion, appossime nucleotide insertion)
		_				
3609	33977	Α	3649	3	1777	NVAGNPARSMAETQSRAGTAG
				1		PGPRTKQTPGTWGSGQAGAPA
				i .		HPPCYIQESRSGFSAPGRARNA\
				1		PGAANPLCMAPGGAEGSGVIQ
				1		REVEGRPRSHSAPMLSLWSERP
				I		PSCVCLGPDGAADFPRRGRGPR
						PPLQDSPASPSAPRCSPARCSRL
			ļ			PL*PRPRDKDAPGTGGRPG/PPG
		1	İ			TLPDSRLECSASRPCGEGCETL
						VQFPDRRGPGCGPLQGPGRGNF
	1		ļ.			ARPQPRLTRAAP\GPTAPAALVS
		1		1		SGGAAVPPRRTR*PLLAGAVEV
				1		ASPRPGSVQSLVPEHPGPFKELR
						NIVLSNSPEASYSAPAN*RPPPA
						EIRRREWQELRGGVLGGGLVFS
						FPPHSCVGSTGAWGLPTWRGV
		1				GSGIQGFFSVPP/SGRETSRGGR
						TATAPWSSTPDCPSHWREPSAG
						SLRRG*GRRDAAPGAR*SRAPP
			1			TRPGSRASPG\GAGEAGVEGEL
						LGPRGQVVTG/PGRPTAPGIYRP
1						GGRRKASAAGSRCATGGSRSSC
						PRRGSRSPGWRWTRWGVP/GR
						RGTLARPAPGPGCPYRRRPGGA
ŀ						PRGAGGRPSTGCGSRSRQWLA
						GQLLPRPSMLGALPGLAPLQPP
						PAPPVPPPPPPPPPPPMPLSAALSS
3610	33978	Α	3650	3	922	NVAGNPARSMAETQSRAGTAG
						PGPRTKQTPGTWGSGQAGAPA
						HPPCYIQESRSGFSAPG\PRETHS
						GAANPLCMAPGGAEGSGVIQR
		1				E\GKAGPDPTARLCSAFGPSGRP
		1				PAC/RLGPDGAADFPRRGRGPR
		1				PPLQDSPASPSAPRCSPARCSRL
						PL*PRPRDKDAPGTGGRPGRLG
						HSLTRAWSAQHPGP/AGEGCET
						LVOFPDRRGPGCGPLOGPGRGN
						PARPOPRLTRAAPAPDSAGSSG/
			1			APPEGCCAPAKDEMTPAGRSC
		1				GGCLAETRICPVARP*APLEKSF
				1		PNVVNPGKKKAQPTLSPSNMT
3611	33979	A	3651	h	542	LPGAGHRRVLDAGGPRGAGLO
2011	-37.7	1	I	Γ.	I	POLPAROVGAVAELHVSGPPG
		1		1	I	AGLA/GSGSGASGVGLGAAGW
	1	1		1	I	GSGPRGVRAEGEGAYSGPGQV
		1		I	I	FPVOGNVGNADAGTTGVGVPA
		1		I	I	GWWPPLPTRLQTLSVASPWLCF
		1		1	I	*AAASARSPPSGLSGE*TLFYTF
				I	1	SFLPPVVIAASPPAGLASEARPC
			1	1	1	
	I	L	1	L	l	FPRFHSYP

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3612	33980	A	3652	I	3063	MSLEVDRSVETMCSGDEILLPD LPKADVADPLWGPPPVQNCLS LARSDSREGOLVL-MESSRNE VVPPGVSYSKDGAKSLKGDVP ASEVTSKDSTTSQFSPISSAEC GDDEKKWDDPI-TRRTCNGS SAPQQDYDKLKAPGGENSSKT GLSPSGMMEKNKVVKREAEAN SINLSYVEPFSVRKAEDKLKEN SDNVLENRVLDGKLSSEKNDT CLPGTAPSKTKSSSKLSSCSSAI MALSAKKAASDSCKEPV
3613	33981	A	3653		847	MENKKVASRGWTCWECDRLF MQRDVYISHMRNEHGKQMKK HPCRQCDKSFSLSHSLCWHNRI KHKGIRQQPDSRRTFTKRLMLE KHVQLMHGIKDPDLKETTRCLMLE KHVQLMHGIKDPDLKETTRCLMLF P*GGNRNKRRQFRSPVPSRSWK NQFWSSGLPKEQSLNH*KS*KS MULRTFSALVAGFTTENLLQFH EHIPQHKSDGSSYQCRECGLCY TSHYSLYMHLFIVHKLKEPGTY FXQNGAGEDROQENKPSHEDD SPDGTVSDRKCKVCAKTFETEA ASNTHMRIHGMAFIKSKRMSSA EK

350

SEQ ID NO:	SEQ ID NO: of peptide		SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
NO:	sequence	нов	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	Sequence			sequence		
3614	33982	Α	3654	854	3009	VNSHSQLLQRE*NT*ESNLQGM
						*RTSSRRTTNHCSMK*KRIQTN
ł		l				GRTFHAHG*E/RVNIVKMAILPK
		1				KIQSDLTSHEISLEEMKKHNQG
						KEAAQRVLSQIDVAQKKLQDV
		ļ				SMKFRLFQKPANFEQRLQESK
						MILDEVKMHLPALETKSVEQE
		1				VVQSQLNHCVNLYKSLSEVKS
						EVEMVIKTGRQIVQKKQTENPK
						ELDERVTALKLHYNELGAKVT
1						ERKQQLEKCLKLSRKMRKEMN
						VLTEWLAATDMELTKRSAVEG
				l		MPSNLDSEVAWGKATQKEIEK
1						QKVHLKSITEVGEALKTVLGKK
		1				ETLVEDKLSLLNSNWIAVTSRA
						EEWLNLLLEYQKHMETFDQNV
1						DHITKWIIQADTLLDESEKKKP
1		i			1	QQKEDVLKRLKAELNDIRPKV
			1		1	DSTRDQAANLMANRGDHCRK
		ŀ	1			LVEPQISELNHRFAAISHRIKTG
		l	1			KKPSWRRGVSNLGEMLVEVYL
		į.				KALMSEDLRKGINQDEFSPTIY
1	ļ				İ	YFPITVFGSEGDLLLGKIRWIQG
		1				AYCLMIGQDVFMDTRLRVSAC
		1			i i	FLKTKMKTVLVVFDQNEDNEG
		1				TVKELLQRGDNLQQRITDERKR
		1	1		l	EEIKIKQQLLQTKHNALKDLRS
		1	1			QRRKKALEISHQWYQYKRQAD
				ļ.		DLLKCLDDIEKKLASLPEPRDE
		l		1		RKIKEIDRELQKKKEELNAVRR
			1	1		QAEGLSEDGAAMAVEPTQIQLS
		_				KRWREIESKFAQFRRLNFAQIV
3615	33983	Α	3655	44	953	GVHNGVEELILVRRMQKSPGP
1	1		1			GEMESGSLEKEPLGTQTGPVPS
İ		ĺ	1	l		E/EYGIGLSQSISTKHPETSPKDS RIRENDVTADGRTTEDHITADP
İ	i	l	l	l		GTTEDSVTADGGTTEDHITADP
	1	Į.				GTTEGSVTADPATTKDYVSADF
			İ			
	l					GTTKDSVTADPGTTENFVTADP GTTKDSITADPRTTENFVTADP
			1	i		GTTKHSITVDPGTTEDSVTADP
		1		l	1	GTTKHSITADPGTTEDSVTADP
1			1			GTTEDETTKHGDTHLL*TTSVT
1				1		AVKPTRLLTPMGIILISLAATTV
1						TVVLFVGLGFIVKECFLPPLNPS
	1			I		TRVIYHPHVMDYSTP
3616	33984	A	3656	200	542	CSPPSTRPGPGP/SGTAWPGPRG
13010	33764	l^`	3030	200	342	TKRSSPSSSSSSSSTTSTTTSSSSS
1			1	1		SSSSSSSAPPRGFSSTRPSPLRR
						LLPPSSSSPSSSSSSPSTTSTTTSS
				1		SSSSSASAGGRRAGTRG
		1		<u> </u>	l	BBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB

SEQ ID	SEQ ID NO:		SEQ ID NO:	Nucleotide		Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid of peptide sequence	*=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence		09/540,217	codon for peptide sequence	or pepude sequence	deterior, (-possible nacieotide insertion)
3617	33985	Α	3657	132	853	EIDKKHRFLVSISLNSPSK*GEG
		1				DTPSRPHRARTGASVVPSPKFPT
		1				SLGRSALSRHPHQTTNPTRPLR
		l				KAGAAAFNAPRAGPLGTAWPG
					İ	PRGTKRSSPSSSSSSPSTTSTTTS
			l	l		SSSSSSSSSSSAPPRGFSSTRPSP
	1					LRRLLPPSSSSSSSPRSSSTGDEA
						AAAAPVA/SRGAGPGA/SAAAA
	1				l	AAAASSSPG/SGAGAGPGTGGG
	1				ŀ	SPGRAASLAGAGAGPAGCSAA
						PPRRLPRLERLARRRAC
3618	33986	A	3658	222	373	
3619	33987	Α	3659	3	513	IPAALSCCCPEWQALV*QILQDS
		1				SCCQSPRVPGHSCGKGTTLCVF
1	l	1				SREWSLVSGSRC\SDGETSCTGR
	1	1				CCNAFLCYDLRFSWLFCTLDVR
1					}	RGVA/GQGGRLGLDLGLSAVCI
	1					HQVWVMGSRCG*QLLAPGRVS
	1					RPRGRERGTHWSCWCRSPWM
	1					GSGWEAHSGAACLSGVFVP
3620	33988	Α	3660	3	463	
3621	33989	Α	3661	263	1020	SGLREPKQLQMLEL*RKMSQLS
						LEG**SSHNM/V*RL*KKCSDYS
					İ	YRDYILSWYGNLSRDEGRTLPS
						ALGR\FWEIARQLHDRLSHVDV
				1		VRSCLQGCCEDLYSLISVT*KLP
1					į.	MPDMKNSQDLLCCT/PCLRNSD
l	ł	}				DEVRFLQTCSRVLVFCLLPSKD
	1	l				VQSLSLRIMLAEILTTKVLKPVV
l						ELLSNPDYINQMLLAQLAYREQ
1					l	MNEHHKRAYTYGPSYEDFIKLI
ŀ						NSNSDVEFLKQLRSVEGTVEKS
		i				GRRCVLVVFNN
3622	33990	Α	3662	1	4314	
3623	3399I	Α	3663	2	492	ISAGVTGTSGLSAEATGIPGLSA
					į.	GVTGKTGLSAGVTETIGLSAGL
1			1		l	SARVTESTGLSAGVTGTIE*SAV
	1	١.				VTETTRLSSGVTGTIGPSAEETG
		1		1	I	ATGLSAEVTGTTGSLAEVTGTT
	1	1		1		GLSAGVTGTIGSSAAGLSS/AP*I
1	1	1	1		1	PSIPAFSGLVFILSCSTKFKAKE
			1	1		WLFFV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3624	33992	۸	3664	1	959	AGLSLMGSI*ACHTGLESSLPV WILSAPSFPPHPVTSSPPISFHLC
		l				KLSLSH/CT*LGTVGALLPASSA
						THVHQAWPQWPATLMSHWNC
					1	YPREGEEIGYLPTSHPTPHYIPV
						LTTSA/HSAAPSHFGQSQAPIRL
1						PPPPGAPSISLSPLPQNLCKGYE
		ł			1	RDPLPSRPPLRAVRSKKQKLGW
		l			1	RLAGPLSKSPDGINLPFLTSPLG
						CLDLSLPPGPGPTVLFSVSLWH
ŀ		l				STKLCQHQSLTGLGGQPGQQG
					i	SSSPSAVFRGSRDVSGVIAQROT
	i	i				SOEKELESGL/CVLTSGAPSPSSF
						HPPYRGTSLFLFYLCILEKGKM
		1		i		VNKRDLCC
3625	33993	A	3665	2	2180	CPOSLIAVEORKPPPTGSQVLLQ
		l		1		PRAAQGTPLPTATPHGTSGDAQ
l		l		1		KHLLQTW*NTWP*KKPGPSPT/
			1			VRRTQDTDQTTAQHPEGAKVQ
	1		l			GHDQFPGGSVHFGCRPAPSPPR
		l				RQG/PLAWHGAGADGFPH/GSP
		1	1			FPSSLTRRCTATPSVLKTSPYRK
1		l				PLLHSCPSN*MYP*PTRPPPSPTS
	1					PTQLSLRT/ANVATCPPLWPLPL
		1				RRHLSQWVPPNWEPGAASGSS
						REHGGI\PAMPQPQCSAPSY/PPT
		1	i			EACLQSADGDQALSKHSADTN
	1	1				AS\RPKPRGSWCPPVTDEDAES
						DRGSGQQQSQRTPAEVLGKPQ
i	1	1				VLERFLLPTQTKQEGSHDEETR
						HVHNCREGSTEKQGRHPLPARF
		1				SPASSKRLL/TPGPSPPAAKRLL
						RQGLLRPAATPCSASGGYLGTR
						QRALGAGALGGCEPTPATGEES
						RPCHLR*PLSPSDSSSLCPLGFA
						K/PHQARNAGLLGASTGMKAT
			l			KWAGACRQRTAKTEAWASSW
		1	1	1		QRVSDTKP/GSTRQKNKDSGSH
			l			PQYQAFDLRLTITAGFSAAEAS
			1			ELEGSCAAATQISSLQVACHGT
			1			SRPHNHVVDDIMNSTAGPPSGV
			1			CGELENVMSGKPTQLVSEMLQ
1			1	1		VR\PSPSGASFQQSLRMT*VSVN
1				1	1	WTPPRPCI*NRP\AAPAETSPAPR
1 '	1		1			TA/STPNASPQGPSARGFVEKW
1		1	1	1	[NGSHAARHPRYKPGTQ*PSGA
		l		1		ASTG/SPGTPPSPALPPCRASSLV
3626	33994	Α	3666	3	426	
3627	33995	Α	3667	3	266	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
]	sequence		
3628	33996	Α	3668	2	1256	CHCGPP/VKVEAYGSQVLKGVL
		1				AQVQLTVGPVGPRTHPVVIFPV
						PECHGIDMLSSRQNPHTGSLTG
		1		İ		RVWTIMVRKAKWKPLELPLPR
		İ				KIVNQKQYHIPEGIVEISATIKD
						LKDAGVVIPTTSPFNSPIWPVQK
						TDGSWRMTVGYCKLNQVVTPI
						AAAVPDVVSLLEQINTPPGTWY
		1				AAIDLANDFFPIPVHKAHQKQF
		1				AFRWQGRQYTFTVLPQGRWEI
		1				NMTKIQGPSTSVKFLGVQWCG
	ļ	l				ACQDIPSKVKDKLLHLVPPTTK
	l					K/EAQCLSGFRREHIPHL\PIYRV
		l	ŀ			SRKAANFEWSPEQEKALQQVQ
	ļ	1				AAVQAAWPLGPYDPADPMVLE
		l				VSVADRDADWSCWQASI/GHK
		l				VGHAQQHSIIKWKWYIRDWAR
		l				ADPEGTTKGQGQRRWWQLAE
		ĺ				RQDSRDREAAIGERQETAVGKT
		Ь.				ARDGEAVCD
3629	33997	A	3669	349	718	AGPEGTTTAECP/I/CQQQRPILS
		l				LRYGTISWG/DQSATWWQVDY
						IRTLLSWKWQSASAKTTIHGLT
		1				KCLIHHDIPHSIASD*GTCFMAK
		l				EVWQWYCFSHSQDSRVQESRG
3630	33998	A	3670	667	960	GIGSCTTHHHPCSFPN
3631	33999	A	3671	1	1371	
3632	34000	A	3672	i	942	MVGKAKWKPLELPLPRKIVNO
3032	34000	ľ	3072	[742	KOHHIPEGIAEIAATIKDLKDAG
						VVIPTTSPFNSPIWPVOKTDGS
						WRMTVDYCKLNQVVTPIAAAV
1						PDVVSFLEEINTSLGTWYAAID
			l			LANAFFSIPVHKVHQKPFAFSW
		1				QG/QQYTFTVLPQDYINSLAL*H
		1				NLIWRDLDYF\LLLQDITLVHYI
		l				DDIMLIGSNDHKVGGAOOHSII
						KWKLYIHDQAQTGPEGTTTSVI
						AOWAHEOSGPGSRDGGYAWA
						QQHGLPLTKADLATTTAECPVC
		l				OOORPTLSPRYGTIPSLPLTKAL
		l		Ì		TLQLKKCSSGPMLMEFTGLAM
		1	l			FPIILKOLD
			L			

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3633	34001	A	3673		1270	MGDPSRRRTCRAMOAK YPLVF KCGVCWGSLDPRCRVASQV WPIPKRLSRGWPFHNAVGRQV SDWKSGQDFADFGTTHQTGF PAGANGRGPLAATLSGPGGG QSAVARLTGEKKNIPGAQYAN RLSPRVGRFINAAGTTGFFTGK RAVSATQLMILCLLPGYLCNGK RKLSAIQGLLDNGSELSLFPEN KRHICGLPWKVGAYGGQKTDR WRHICGLPWKVGAYGGQKTDR WRHICGLPWKJGAYGGWFIDK WRTYDVCKLNQVVAPIVAAV PDV/VVSLLEQINTSPGTWYAAI DLTNAFFSIPVHKAHQKGFAFS WQGQQYTFTVLPQGRWEINNT KIQGPSTSWKFLGVQWCGACQ DIPSKVKDKLLHLVPPTTKKEA QHLTGLFGFRRKVIPYLGVLLC PIYQVTRKAASFQWRPEGEKAL QQVQAMQAALPLGPYDPAGP
3634	34002	A	3674		1978	LTIVAVNLSLILPQGDLWPFTRV THY*GKGNDQTTGELLDTOSSEL LIDGYPKRHCCPPVKVRVYGG QVINGVLAQV*LTVGPVGPRTH PVVISPYPECIILSSWONDPHIGF LTGRARAIMVGKAK WKPLELT LEPRKIVNKKQYHLLGGTVEISAT LEPRKIVNKKQYHLLGGTVEISAT IKDLKDTEA.VTPTTSPPNSPIWP VQKTDGSWRMTVDJYCKLNQV VTPIAAAVPDVSLLEQINTSPG TWFEWSPKIKALQQVQAAVQA ALPFGPYDPADPMVLEVSVAD RAJWISLWANAIGESQRRPLGF WSKALLSSADNYSPFERQLLAS YWALVETERLIVGHQVTLRPE LPIMNWVLSDPSSHKVSGAQQ RSIIKLKWYIIDWVRAGPEGTS KLHEEVAQMPWYSTPATLPSLS QPALMASGGVPYYQLTEEKT RAWFTDGSARYAGTTGKWTA AALQPFSSRTPLKDSCECKSPHH PVIAQWAHEQSGHGGRGGGYL WAQQHGFPLTKADLAMATAE CPICQQRPTLSPRYCTIPQGDQ PATWWQVDVMGPLPSWKCQR FVLTGIDTYCGYGSAYSARMAA KTTHIGLTECLFHCLGIPHSIA SDRGTHFMDKEAPSASVLGLA LALLAPQLADSLLEDPVIVKGT DEAEYFQSVREEPDSGVKRKK

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3635	34003	A	3675	T	746	MGKIVQPEKAVSAKAGVCLKG
		1				CDCSEYKVQCEWQDTSPKYLG
		1				IVLSFGEEPVTHLRWDLHAWSY
	1					ALSKVISTICRRGKFSEFKAHTA
		1				PVRSVDFSADGQFLATASEDKS
1		1				IKVWSMYRORFLYSLYRHTHW
				j		VRCA\KFSPDGRLIVSCSEDKTI
		l				KIWDTTNKQCVNNFSDSVGFA
		l		l		NFVDL*PPSGTMP*PSAGS\DOT
	1	1				VKVWDVRVNKLPTALPRMVY
		1				YGAKCHLWGCWSFTENSELSF
		1				QLFCTSIPIWF
3636	34004	Α	3676	5	812	AAGSAGLPATPOPRARRVGRR
		l				RLGPGARGAGGAGGAAGCRAL
1						RATARAAGSOPGPHSPGRTARS
		l				ARK*RLRRPESNKVRVCGPHSP
						APRTPPSSPGIOHAGKPRARRPL
	i				1	PPPGAGVGLGIVPGLGLGRAGA
		l				DVAGRVGPGAGVPGCCREGAR
	1	l				RPGSGRRAAPVLSPLC\PGLQTA
	i	1				RAAAGPAPGA/GWP*VRRLEPA
						EALPSGMFMMRKSCSVALTSSL
	l	l				SSSPSSSSSSSSSSSSLTRPDVS
						PRVTAATGDMYRGSFSGLTKA
						LRTWPR
3637	34005	В	3677	1	1071	
3638	34006	A	3678	1	169	
3639	34007	A	3679 3680	3	189 352	CIVIDII IVI TATCODURDI (OL IVI)
3640	34008	A	3080	3	332	SKHNLKLTATSQPHRPMQLKP ACVPPVLSSPHMWGRSDTSEGP
		1				AH*PPA\AWRVCVVLGL*ASPP
						AKLQAQHQAGSTRPVDRQAPS
						VLTAPPLVWPPFPQGICSKWGA
	1					OHGKRGOGH
3641	34009	A	3681	8585	9026	ERYKFFSAASPNILILLTFFKIVV
3041	34009	^	3081	0.505	9020	RPLITKENLYLEILIRHSLLCSVL
		l				TLVCVFCCPVFIGSCSSKRLTTA
		1				WTHSTGLCAAMSSPRPGGGGG
		1			Į į	KGGPAPWAGKRAGSGG*GEGR
						GKERVCGVQAPSVPTGVGMGG
		1				ORRAGVGGPRAAP
3642	34010	A	3682	2	484	VINAOTOUTKAAT
3643	34011	A	3683	1499	1793	IHSIESSPIPHWIGGLRLMLCIVT
[1		1		RLNFEICLVKHFIKQCKVVEHT
1						QQYEWHRVLHLKKK*QALNLK
1		1		1		KNLQT\GDKKL*VSSLVHGETN
						SCRSKALAL
3644	34012	С	3684	1	1044	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3645	34013	Α	3685	8504	8970	ERYKFFSAASPNILILLTFFKIVV
				1		RPLITKENLYLEILIRHSLLCSVL
l						TLVCVFCCPVFIGSCSSKRLTTA
ŀ				l		WTHSTGLCAAMSSPRPGGGGG
ŀ		ĺ				KGGPAPWAGKRAGSGG*GEGR
						GKERVCGVQAPSVPTGVGMGG
				ľ		QRRAGGGEGKGALARRLGGG
3646	34014	В	3686	1	2178	
3647	34015	Α	3687	I	2424	MLTVIHSEMQAAKVSDGNEELI
		1				GKWNLLGIERPWGPRRDWSGL
		ł				HGPGPGTPTARPRPLRDSSQNT
						WRLQLKPRLKGGPGAQNARM
						NEAWQPLPRFQRIYEKTWVPW
1		1				QKHDAGAEPSQRTSTRAVPRGS
l						MELEPPHRAPRAVRRVPQFSRF
				l	ŀ	QNGRSTSILHPVPGKAAGTQLK
}				1		PVRADLVAALYKATGAELPKA
1						LGAHPLHQCPLDVTDELLEKIA
ļ				l		SRSQNIIEINISDCRSMSDNGVC
				ŀ		VLAFKCPGLLRYTAYRCKQLS
				l		DTSIIAVASHCPLLQKVHVGNQ
l						DKLTDEGLKQDNQPQCIEGNFE
	İ	İ		ŀ		SRMHAQGRTLVQERPKKTVNFI
						TVCLLGPVQAGSKGQGRVVNG
						KVLTSTANLRRISVDGKSEKSV
						KDAEKAFDKIQQPFMLKILNEL
						GIDGMYLKIVRAIYDKPIANIIL
l		i				NEQKLPWVVDGTGRCGAGGS
						VTGEARAMQ\GPQWGKGRLRH
1						GGLQVPIPALQGGS*GPARN*A
						QQLLAQRIKYL*IQLTRDVKDL
						FKEN*KPLLKEIKENTKKWKNI
						PCLWI*RINIVKIAIL/PKVIYRFS
						AITIKLPLTFFTKLEKKTTLNFI
		1	1			WNQKRACIAKTILGKKNKDGG
l						IMLPDFKQYYKPTVTKRAWYW
						YQNRYIDQWNRTETSEITPHIY
1			l	l		NHLIFDKPDKSKQWGKDSLLN
				l		KWCWENWPAIYRKLRLDPFLT
			l	l		PYTKINSRWIKDLNVRCTTVKI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codnn for last aminn acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codnn, /=possible nucleotide deletion, \=possible nucleotide insertion)
3648	34016	A	3688	453	1508	KAPQAPNINSYCLQVEECCQKG ISVDLSTGMTSTGVVP/HYNEQ VAGEKEEETNSVATLSYSSVDE TOVRSLYVSCKSSGKFISSVHSR
						ESQHSRSQRVTVLQTNPNPVFE SPNLAAVEICRDASRETYLVPSS CKSICKNYNDLQIAGGQVMAIN SVTTDPPSESSFEYGPLLKSSEIP LPMEDSISTQPSDFPQKPIQRYS SYWRITSIKEKSSLQMQNPISNA VLNEYLEGKVVELYKQYIMDT VFHDSSPTQILASELIMTSVDQI
						SLQVSREKNLETSKARDIVFSRL LQLMSTEITEISTPSLHISQYSNV NP*RGCFHYCLAFT*T*SNTLSI YSENVQEGLVKGN
3649	34017	С	3689	57	230	
3650	34018	Α	3690	2	123	WWKV*KKYSGFKVFL*HQH** PRRPLQSLFS*MPWKRIAK
3651	34019	Α	3691	94	360	LMSLLTSPHOPPPPPPASASPSA VPNGPQSPKQQKEPLSHRFNEF MTSKPKINHCFRSLKRGVSSAPE SCLSGVLWLHVWFCITNFVCE
3652	34020	Α	3692	1	2037	OCEOGYEWENT WICHTHIT YEE
3653	34021	Α	3693	2	1079	NLSKKYQPKKNSKEEEEYKYTS CKAFISNLEMBIDYAGQHEVIS ENMASQIIVDLARYVQELKQER KSENDHRVSGASRRAPLPGPFR RLPFTPDVGGEEAAANQAEQ "YPSLKWNSKGKTNGTRNOTK CGKEHSPTLHQSRQGTVIQSAN RSVA*SYRAPLHPSPH*KLAP* VPAFSSSRVFPMLSSFSL/YISTD DQEGLYSLYPHKCLGKELPSDK FTFSLDDSQLVEAYKSGFEPPG DIEFEDYTQPMKRTVSDNSLSN SRGEGK PDLKFGGKSKGKLWP MTSKRHCHCFRSLKRGIQPPDG MTSKPKHTCFRSLKRGIQPPDG MEKQDTMASSFTFSLSLDYEM PVIEKAE
3654	34022	A	3694	I	215	MAQDYGAMGDLVLLGLGLGL ALAVIVLAVVLSRHQAP/C*PPA FAHAAVAAHSKVFSNIVRERV KTOEAERA
3655	34023	Α	3695	1	208	MAQDYGAMGDLVLLGLGLGA\ ALAVIVLAVGLSRHQAP/C*PPA FAHAAVAADSKVCSDIGQRTC RDATPT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nuclcotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
3656	34024	Α	3696	Î	164	MRYRYIPVRMAEVRT/SDETKC
		ı		-		W*ECGATGTFIHCWLANIQQHT
						LSRLFTCLCSC
3657	34025	Α	3697	146	659	LAGPRCTTSLTPSEGG/LPPPDSL
						GYTVHPPDSQGHTGPLPAREGT
	į.					GSHRFGVE/VRQRRWERGEAPL
	l .					LQLSPPAGRPPRRPHPCRPQHLP
						SAAISEAATARGPRNRSQAAAA
l						AADPDNLRVARG/PRSTRSSAV
		1			i e	DAGPPP\SASPGFP*SSSQQRPSP
						EKTGSEVYSAYIPANC
3658	34026	Α	3698	32	376	
3659	34027	A	3699	1	2148	MALSPWTPGLGAGEKLVQAAA
l	1	1				VSTGPSLELCTLPSTLGSSVAVE
1	1					ALEQLEVVECVRDARRLNLFEI
	1				l.	NTIKMRITRTENEIELLKKKITD
		ŀ				LTKYNEALGEKQEELARKHAR
	ŀ	ľ				FVLSLNQTMEKKATTTVYINET
		1				YTKINLKREDIALQKKCIQEAEE
						LMEKERAEYLIRKQELTAQINE
		1		ĺ		FENTREVKRMETYQKK/QRIG*I
		ľ				TN*NVKNKRNSY\FSAAVLSDH
1						NLEIARLHESIRYWEQEVSELK
	İ					KDLAILEAKLCFFTDNKEKLDD
ŀ		1				ISNDEKNEFLNKIKQLVETLHA
						ARMEYKDLREKMKTLARQYKI
						VLSEEEKAFLQKQKIHDENQKQ
						LTFISQKEYFLSQKRVDIKNME
						EGLITLQELQQVILSFMSSVYSK
						PNLSHSRGLTCCSFPLYLQMMT
	i	1				PFPCVITQWKMACLRKKHARW
	l					TAKIKAEIQAITĒKIQNAEVRRI
						ELLNETSFRQQEISGFVAQIEKL
		1			1	TTELKEEEKAFVNKEKMLMKE
						LSKYEEIFVKETQINKEKEEELV
		1				EYLPQLQVAEQEYKEKRKLE
					1	ELSNIITEIIWGFLFEQEDVKQEL
	1	1		1		QQLRDQESKKNKDHFETLKNL
		1	1	1	1	ENGFYINDQKADLLLLENKKLK
		1				EYILYLKNNIEKYREGQEALMH
		1	1			TSSDLSRQLIAQEGLLQVEEQGI
		l				QWWIRQSPKASQVGKPTVQPS
						VCGQRPKSPCQTTGVNPRVQK
	L				L	LKNLESNVRGQEASSTGERGIL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3660	34028	A	3700	1	2658	MQAPYRCQRTGWLQQKRLKA GLWGLESSSWSLGPLGQAAQQ ELTSAPGGFELPPPQAPERPTA GGSASLGPPLP/PGKLSEVPEPS RPGRPREPSTWAPPGGFGASS EAGPHLPIPVTSNAPGHAGGW. GAPSHQNHASPCTGGFQPAGE LRQAGEGFPSWGRRGSCRTC SVVLGHTEPREPAHVLVR\GN PGSPVGAAWGMSAGHPRAPG AORGG*RSPGLRE
3661	34029	A	3701	31	556	AQUOG ABIGERE
3662	34030	A	3702	3	1394	RKKELQHKIDEMEEKEQELQA KIEALQADNDFTNERLTALQEN GYTRAKESDFSDTLSPSKEKSSD DTTDAQMDEQDLNEFLAKVSL LKDDLQGAOSEIEAKOEIQHLR KELIEAQELARTSK QKCFELQA LLEEERKAYRNQVESTKQIQ LLEEERKAYRNQVESTKQIQ NEIASARDELHSARDEMWLVH QAAAKVASERDTDIASLQELK KVRAELERWRKAASEYEKEVT SLQNSFQLRCQQCEDQQREAS RLQGELEKLKREWNALETECH SLKRENVLLSSELQRQEKELHN SQKQSLELTSDISILQMSRKELE NQVGSLKEOHLROSADLKTLLS KAENQAKDVGEYEKTOTVLS ELKLKFEMTEQEKQSTDELKQ CKNNLKLLREKGNNPSILQPVP RAIHBPIPGFPDWISISIVERKK PWPWMPMLAALVQVTAIVLY

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3663	34031	A	3703	I	1133	LEEKEQELQAKIEALQADNDFT
5005	15.051	· ·	5705	ľ		NERLTALOEHLLSKSGGDCTF1
l						HOFIECOKKLIVEGHLTKAVEE
İ						TKLSKENQTRAKESDFS\DAVSP
l						GKD*GSDDSTDAOMDEHDLNE
1						PLVKVSLLKALLEDYRGGYRN
ł						QVEESTKHIQVLQAQLHRLHID
						TENLREEKDSEITSTRDELLNAR
						DEILALHQAAAKVASERDTDIA
						SLQEELKKVRAELERWRKAAS
					•	EYEKEITSLQNSFQLRCQQCED
						QQREEATRLQGDHTDEAADLP
						LSRHSVSDPGVSCTQEEIQEAR
	1					GLTLLCFSKIKCSQKQSLELTSD
						LSILQMSRKELENQVGSLKEQH
						LRDSADLKTLLSKAENQAKDV
	1					QKEVKRKDIMSPIMVGLKAKS
3664	34032	Α	3704	1	540	
3665	34033	Α	3705	1	280	
3666	34034	Α	3706	2	416	
3667	34035	Α	3707	309	908	LPSRGAGLGTCRPPCLSLPLLP
						WAPVLPEPPRRVPPPAPRRPVG
						STTQGLRSASTRR/VDWQAAPP
						AALVWDPLGEASWAP/GVWCA
						AIDLANAFFSIPVHKACQKQFA
						FSGQGQQYTFTVIPQRYISFPAL
						CHNLI/RRDIDCFSLLVVHFAWK
	l					EKWSDVRLGTDSWAAASGLA GWSGTWKKHDWKTSPLVIHEO
						KFCFLFP
3668	34036	A	3708	1	2973	KFCFLFF
3669	34037	В	3709	1	1053	
3670	34038	Ā	3710	li	1178	
3671	34039	Ā	3711	3	247	DCLRVLWCPPV*F/ORSPSLOOP
	1	ľ.			[· ·	L/RPGFEPLVGRHLMRPARSWR
	1	1				POPSSASAGLPSSPFRDGCHRFR
						ASWALGGRAAEGEVAI

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3672	34040	A	3712	137	2176	LKNPPOTHPRRGHLLLISVWGH
						ILRACGAWOEAKPKAKWPOIP
1						EEKEEGQAPRACTLPGCWRLL
ŀ		1		1		RRGOEEKEENWVPPACTLSGC
				1		WRLEAVROOOREGDGDFGAAS
						CSDLAFRCASSQNPRSLEPVASS
						PERRRROPSRAPLGWALKEPGS
		1		l		ERSPPLLSCVEALOPPFLLGLGS
				l		GAFCLTRGEKGSPDODPFCLHS
						PWMLEAGGSDAATARGDFGA
1						ASYSDLAFRCASSOSPRSPEPVA
1						SISERRRRQPSRGFQILRSSGAFL
l				l		LDREHVCLASSASTTGLGSPRP
ł			İ			SWSHOVASNKGLKPGLRGCWS
1						DGERGTTLEDTRVLLSNPLLLR
						KGGRKVSTSRLMQLCSVVEKY
	ŀ	1		l		CPWFLDQGTMNIEIWEKVARA
		1		l		LKKAYRDGAEDIPINIWSVWAL
						VHPTLEPFHTDHDEEESEEGE
				l		YNEVTKEVTEQFCLPAKAAKE
		1	İ	ŀ		GGNPSLTSPOOLTTETEAEIQLI
	i			l		EKQVHKAQINRIDPEKTLDLLIF
	i		İ	l		PTQHSPTGGVVQEQDLVEWLF
		1		l		LPHSNSWTLTPYLDQIATLIGN
		1				GRTOIVKLHGYDPGKIIVPLTK
		l				AQIQOAFINTLNWOTHLADFM
		l		i		GVLHNHFPKTKLFQFLKLTNWI
				l		LPRITKFKPIECSENVFTGRSSN
				l		GKASYSRSKNKVFQTSYTSAQ
						KAELVAVIEVLTAFEMPVNVIS
				l		DSAYMAHSTQLIE/TAQL*FHTD
3673	34041	С	3713	1	784	
3674	34042	Α	3714	87	447	AVQRRSGVGPACLSCGSANPGP
				1		PPGTSPGAGAAPGGGRWARAK
	l		1	l		SGPESPPGT/GPPQPA*APQ/AAG
			1			PKTRAGVSFLSPPLASSPGHANF
						GPDSFLGDGVMRQA*RSENKQ
1	l	1				DPA\GTPGTWVR

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3675	34043	Α	3715	3	1435	RGPSGPRTVSPSPAGASSVGGPF
						VQAWPCSLCVGSLEPRGSIGGP
						PKGLOLWGPRASWFLGDYACP
						LLASAPVLAACKTLCQTPAVPA
						SL\G*RPLVAVKTHVAAQPFLRI
						KHLAAVLADKSAPGLRPVCGT
						A/GFAGYLCLPHSLPSPDG\EPV
						DVSTLDSAEYCOLGLGGICRGP
						GR*EGGHGY/RGSEKPHSTYPSS
						PSLSG/EPENRG/DPGVAQEP*P
		1			i	PPREQAGPFSPFVILEAAPFSAG
				i		ACFPGSEAPGGSSPPN\GSAVGL
						WRGRCPPGPRSL*RIAAAWPEK
						RCLDSWKG/RRDGAARGVGTA
						ATFSPPFASRLVLPGEASLGTPG
	ŀ					VVFLLRAGEPSASGFPGPAWRE
						STAGASGGGCCGHGPCSGLRA
				i		AGLPSGAGSW/RGDCCHLGMG
				l		EDPLG/PW*SSGTPASARGSOEV
			ļ			PAT*GRAGGRAARHPQGARLPS
					İ	GPPG/EPGSPGFWHRKESQSTLT
						FLGAQGSSSPLADLGSLGASAG
3676	34044	A	3716	I	756	MNDAGNHHSHQTNTRTGNQTP
			ļ			HALIHKRKLINENTWTQEGEHH
						TLEPFGGTTDRIVSPSHTRSPDM
						AIANFQSSGCSVVPDTIPRPQYQ
						CRSRHSVLLTSNLTVPMQSCVK
		l			İ	PPYMLLVGNIKIWMNNQTVRCI
						NCHVYTCITSHFDSRKSVMLVL
			1			AREGIWILVTLPRPWESSLSIRLI
		l				NEVLQRILKRSKRFVFTLIAVIM
						GLITVTALATTAGMALHQSVQ
						TAHFANDWQANSNQMWNSQQ
			1			GIDQ*EHMDTGRGTSHTGAFW
						WNNRQNSFPFPYSQSRHGNSQF
						PKFWVFCCPRYHPSPSV\QCRSR
		1				HSVLLTSNLTVPMQSCVKPPY
						MLLVGNIKIWMNNQTVRCINC
						HVYTCITSHFDSRKSVMLVLAR
1	l	l	l			EGIWILVTLPRPWESSLSIRLINE
	l					VLQRILKRSKRFVFTLIAVIMGL
1		l				ITVTALATTAGMALHOSVOTA
1						HFANDWQANSNQMWNSQQGI
						DOILAAI
3677	34045	A	3717	3	131	
5511	12.0.0					

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-possible nucleotide insertion)
3678	34046	A	3718	2	424	CGRKSRGTALPTGSSPQSGPAA
						PGHSAASALHPTP/SPPPHPL\PP
						AATGDIDGNRYPATPMTKYPS
						ASARRPVHRPTCSGGGSHTNHA
		l				ESLPPLTPLEEADTHPPGGSQ*T
		1				RPPHCIRTGSCLPPPREAPYTRR
						ERRRHPP
3679	34047	Α	3719	1	418	
3680	34048	В	3720	361	1371	
3681	34049	A	3721	I	469	PGTCRGSTGQP*EACWRSP*SV
						RNTRCPVREEPASPGWSSCLTS
						PSARGWWACS*RLPSSSCPGST
						AGSSSGTLCREAAPCHR*AACS
						DGKPPGMPRSTRRLGPSGARSG
						SARRCPCGDGPESLRGHAPARA
						ATQAPDPSTQSSASSATPRAPPL
						L ·
3682	34050	A	3722	117	871	GPQSSAGNAGPQRRRTTLGVPR
						TWHPGPAA*AGNSCHISFYSSR
		1				FQPFLGVTSVLRGSSVSVSGIPD
		ì				HLGQPRSSQEPSRPENAAAQM*
1	İ	1				TGCPGYAGCTVA*MKGRAELQ
						GLRTIAAQPGQWLTLLPRCPST
		1				RRLGPSGARSGSARRCPCGDGP
						ESLRGHAPARAATQAPDPSTQS
					1	SASSATPRAPPLLGLCGGGC*G
	İ					DRRSQQGTE*A/VAVPGMLGGP
	İ					SPFSQPEHPSAFAQPSSCLPLGL
						DFKLLIPSQ
3683	34051	Α	3723	110	1017	EAANEPKHLHQLRHAGLGQHR
					l	QAPRPQGRPFARPHQGQDQTD
						RLHHLQGGGRHGARGHLHQA
						GAGQSAPAPKGAHVQGPCGCH
İ		1				ESTGPVEH*SHGERPKHRCPRP
					'	AL*EHGHENPHK*SSPHDQR*Q
						TADPEGDN*SQCCPTAN*IPLRK
						LWLRG*DLCGRSHGQQ*PHQG
						W/HLDAQLLTPASSSTLCPTPLQ
		1				QPLHQLRHAALAQHRQSPPAA
			1			RT\PLARPHQGQDQPDRLHHLR
						GGGRHGARGHLHQAGAGESAP
						APKGAHVQLVSKQLGGVAAEA
						HVDSSGLWVSPGPRHN*YKSKS
	L					SRL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Antino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3684	34052	A	3724	T3	1092	LVEPGRLLEAQGFDKNKR*RRR
						GRVCGRGGEAPAPGOGOGOPD
l		1				*NKGKEEV*NSSE\EESSEVSLP
	l					KTSREOEIPSLACEFKGDHLKV
						VTDSQLQDDASGQNESEMFDV
						PLTSLTISNEESLTCNTEPPKEG
		1				GEARPCVGDSASTPKVHPGDN
	l					VGTKVETPKNFTEVEENMSVQ
	l					GGLSESAPQSNFSYTQPAMENI
						QVRETQNSKEDKQGLVCSSEVP
		1				QNVGLQSSCPAKHGFQTPRVK
		ŀ				KLYPQLPAEIAGEAPALVAVKP
						LLRSERLYPELPSQLELVPFTKE
1			1	İ		QLKILEPGSWLENVESYLEEFD
1						SMAHQDRHEFYELLLNYSRCR
						KQLLLAEAELLTLTSDCQNAKS
						RLWQFKEEQMSVQVF
3685	34053	Α	3725	182	771	QTALSCARHGRSAAFVWRPNR
			1			APVWRSGFRGVAAGSALVHST
		l				ALPSRRQPPERRSEHDCLRCRA
						LCGTKPQGLSY/TGP/WGLGKV
		1				PEAAAALDLGVH*PLFHLPLLD
		1		Ì		SESRKPGRGLAAPPPMPARWGL
i		1				SCLEQVGHTRKEGGGQGCRPW
						PPCWSPVSGTRGGPITTRLRRGS
3686	34054	С	3726	769	981	AALHVRASYCLMENPPEPPSIV
3687	34055	c	3727	70	197	
3688	34056	Ā	3728	1	158	LGSVSSFASCTLGAPGYSPTAP
		1.		ľ		VAL*SVGPWGRIVKVPGHPGS
						WEMHFIISM
3689	34057	Α	3729	229	496	VTGLQNLVLSIVTESGKTHLLSF
						SSHGLEEIISQLPGCSGTLTVRP
1						QGPT/GSQGNRGCDRVAQGSQ
						GAGGERGDRSQAPVPAPARDS
3690	34058	Α	3730	167	769	FLTRETGDPTGRSSSHGKHPVA
						VFP**PTRPP*TIWEITHGCGRR
						AGRCPGTGPDGP\SGRGGPRCW
						PSGHLAATGGLGPSCGRLGAN
	i					RGEAGPAGFTVCSPLSGWRTPY
						THHFPASRMSWHLDYASPRTY
						RSQGNRGCERVAQGSQGAGGE
						RGAGSQVPVPAPARNKDPAKR
				1		QKPRPPLLSSPTARLIGLFPRAD
						SCRSC
3691	34059	Α	3731	234	543	ALDQVASLPIMVPASKQNTATS
			1			CCRLGYNSFDLGPAAATIFFPSP
1	1	1	1			AMVISQLPGCPGTLTMRPQGPT
	1	1	l			/GSQGNSGCERVAQGSQGAGD
	L			L	l	ESGDGSQVPVPAPARD

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
	of peptide	hod	in USSN	location of first	eodon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3692	34060	Α	3732	I	3695	MGKRSFERVLVDKCDSGRSCL
		i		1	l	RKQHENECAFIQILDTQSLMIPG
						QRGSFRLADSQHTDRVLCTLM
i		ĺ		ĺ		AEKWDRKALSYTRNSFRAQIRL
						RKTRFQGKGCMICKKSRVLPY
				1		QAAYVSQHGSACQPSSHLPSVG
				l		SLSSTGDDEEEEEIVHMGNAIM
						SFYSALIDLLGRCAPEMHLIQTG
						KGEAIRIRSILRSLVPTEDLVGII
		ĺ				SIPLKLPSLNKDGSVSEPDMAA
				i		NFCPDHKAPMVLFLDRVYGIK
						DQTFLLHLLEVGF
3693	34061	Α	3733	I	2523	MKQFLLYLDESNALGKKFIIQDI
						DDTHVFVIAELVNVLQERCHTR
						LGYTEFLVAWRVTFGLCVEAV
						TLHLKYQILIRGLLEMMSFSDA
		l				DILKQLPVTVPGLFPASLSPSSL
						LGNSPPSWLRHNSESKVSAVSS
						PSATKTLSTGIGKLDPGHKEMA
						EESELLKNKMQAPPLSRCPESQ
						KCQHQLRLHHWKPSVRHQVKR
						RSPAVLRSAMPPADCPAVLEAT
					*	TATHPEKGTALSKHLPSSDSMS
1		1				LKVDVEALENSPGATYIWKGG
						KVTRDSQPKEQGKGDLKKKKK
		l				GKLPKNYDPKLTPDPERWLPM
					1	QECSFYQGRKKGKKKDQMGK
						GTQGATAGASSELDARKTVSSP
		l			1	PTSPRPGSAATLSASTSNIIPPRH
						QRPAGAPATKKKQQQKKKKG
						GKGFPVLREITVVKVDTLVVFQ
						ILEERLSVFHIQYDTSYPFSTVDI
						EDHECAVWLLLRKSKSDDKTT
						RLEAVREMSETHHWHDAEKAF
						DKIQQPFMLKTLNKFGVDGTY
						LKIIRAIYDKPTANIILNGQKLE
				l		AFPLKTGTRQGCPLSPLLFNTV
				l		LEVLARAIRQEKEIKGIQLGKEE
		1		l		VKLSLFAGDIIVYIENSIVSAPKL
	1	1		l	1	LKLISNFSKVSEYKINVQKSQAF
			l			LYTNNRHTESQIMSKLPFTIATK
				1	i	RIKYLGIQLTRDVKDLFKENYK
				l		PLLNEIKEDTNEWKNIPCSWVG
	L					RINIMKMAILPKVIYRFNAISIKL

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3694	34062	A	3734	1	6208	MILDOAFKYITELKRONDELLL
						NGGNNEQAEEIKKLRKQLEEIQ
			i			KENGRYIELLKANDICLYDDPTI
	İ			I		HWKGNLKNSKVSVVIPSDQVQ
	ł			i		KKIIVYSNGNQPGGNSQGTAVQ
				ŀ		GITFNVSHNLQKQTANVVPVO
	ļ.		1			RTCNLVTPVSISGVYPSENKPW
						HQTTVPALATNQPVPLCLPAAI
				ŀ		SAQSILELPTSESESNVLGATSG
				1		SLIAVSIESEPHQHHSLHTCLND
				I		QNSSENKNGQENPKVLKKMTP
				1		CVTNIPHSSSATA
3695	34063	Α	3735	164	415	EYWGWLLRRINIILTGNCLRG/
				Į.		WPSLLPQAEESLSPQTKVERLK
				l		AAWIEEGILPLLGMRKLFLLAR
						KVHQSLQAQCPQLHQGPPT
3696	34064	Α	3736	I	886	MLDLPWFNVEEGIQRLREIGML
1				1		EWLSHFRPTRLSREDPEDIPFTN
ļ.						TLPNKFVRGVPASLKSSFIGLLC
						MPDLTKTVGSWRMTVDYHKL
		1			-	NQTVTPIAAAVPDVVSLLEQIN
	Į.					TSPGTWYAAIDLANAIFSIPVHK
				l		VKDKLLHLAPPTTKKEAQCLV
		1		ŀ		GLFGFWRQHFLHLGVSLWVIY
		1				RVTLKAASFEWGS\EQEKALQQ
		1		ľ		AG\QAAVQAALPLGP/HKDPAD
		1				PMVLEVSVADRDAVWSLWQA
		1				PIGESQQRPLGFWSKALPSYAD
1						NYSPFERQFLAYYWALVETERL
	21000	١.	0505		1016	TMG/HQVTT*PELRIM
3697 3698	34065 34066	A	3737	1	1815 988	MPAEFFORCSVIMVOLPWKEA
3698	34066	l ^A	3/38	1	988	HVERPHGERDYTPDLOPDMWE
ļ		1				KFPGLRRALRPVVKTLLVOLEY
l						ROAEKCEKRDWPSLPDYIFLLC
l		1		1		WMLPALEYRTPSSSVLELRLAL
						RAPOPADSLLWDLVIVPITSLKS
l						WQTPRGEVEGVTHEEICASLKS
						LAVALLSMSDLTVGTPVTQPQT
ľ	Į.	1		1		LNTMGIIGSRGGRGOVAALNR
	}			1		OROVPELIIGIDILSSWONPHIGS
l		1				LNGRGYINSLALCHNLIRRDLD
l						RFLLPODITLVHYIDHIMRLDSV
						KDKWLHLAPPTTKKEAQCLVG
		1			1	L/FGFWRQHISHLETAL/RPVTG
1	1				1	LWWKLNI*LWAIKSPCNLNCLS
3699	34067	A	3739	26	318	RTAWMQYSPLHSAYGRVPTVT
5099	34007	l^	3/39	120	3.0	SSH*LLPLRSHPRDSRPAPCP/RA
					1	GPARNROSSA/SRNRSPRRRNPE
1	1				1	ASRGRPPGRGVASPAPSPPTPRE
	1				1	TRTAATRRP
			L			IKIAATKA

sequence 09/540,217 codon for peptide of peptide sequence deletion, \=p	n, /=possible nucleotide ossible nucleotide insertion)
sequence	ossible nucleotide insertion)
3700 34068 A 3740 425 588 IIWSVPFA	
	PWRRRGHAGSRCSRR
	RRNELSTAALGAARG
HARIWRE	EAGNWP
3701 34069 B 3741 465 1623	
3702 34070 A 3742 667 960	
	TSSQHSTGCHAKPAIT
	VFFQGPGVLQSVGGK
ASQADIII	LGLSPVSAIFQLYDVS
FPPGKQG	GRPGLGSAGRIEVARD
CGMLWK	QRGYLISSSQPIKNGQ
QVSDLFE	AIPEPKSLAIIKISGYS
TLETPES	KHNHFTNTLAAIDLV
NAFFSIA'	VHKVHQKQFAFIWQ
GQQYTF1 GQQYTF1	TVLAQGYINS/PPALC
HNLTQRI	DLDCFWLLQDNTLVH
YIDDIML	IRSSEQEAANTLDLLV
RHFCATO	GWEINPTKTQGPSTSV
KFLGFQV	VCGACQDIPSKVKDK
LLHLAPL	ASKKETQRLVGLFEF
	HLRMLLQLIYQVTRK
AARFEW	ACTDGLMRSPYDQLT
KEEKTRA	ARFTDGSTQCEGTTQK
WIAAALO	QPLSRTCLKDSVHQR
VSSAEED	FNNQVDRMSRSVDII
HPLSPAT	PVITQWVHEQSGHGG
RDRGHA*	WAQQHGLPLTKADL
AMFTAEG	CPIFQQQRPTPSPQYG
TIPQGDQ	PATWWQVDYIGPLPS
WKRQRF	VITGIDTYSRYRFAYP
SFNASAK	STIHGLMECLIHSHGI
PHSIAFNO	QGTHFMAKEVWQWS
HAYGIHV	VSYHVPHYPEAAGLIE
LWNGFLI	KSQLQYQLSDNTLQG
	KVVYALNQCSIYGTV
	SRNQGVEVEVALLT
VTPNDPL	/GKY*LPVPVTLHSDR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X-Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3704	34072	A	3744	3	1197	TLOPGTGPRAGTGSSSPSSPG TGSVPGAGPGANSVVIPGADS GVRAGAALAPGLC*VKLLGQM SPPGGALGPHNARQSAVAGGF GRARRRGRIEF-LQGTWWSGPG QPLGAALQTATGPVVMNGFLR *TWHIEGHSRAPCPR-WGWF* TYSGEKPLPAVQPSSSSVF*SL QQCPFFLGVPCQACSSACPLL F*GL*W*PGVHEDGY*ASPAGSA LTWP*LHHDPPPSSGA*SDATG PGGPGSALAGFQQLGSGGQVL QQGQLGSQTCRGGSPGRRHC* ASSWG*G*AGRLLPWA**PPAR SAGSPHRLRGLS*ARPGGCAPR CRAAGGAGP*SAPRTGDGDV GQLGERE*EAHPARVGQWGW GGJGERE*EAHPARVGQWGW GSSNRRFRIDT
3705	34073	Α	3745	1	98	
3706 3707	34074	A	3746 3747	439	1053 751	EGDLVFPLGRGMLRLVSFSKMF KLLKKTMDYGSGSPSVSGHIPL POACGPPOLVCSRRVRGGPSP HSVPGSRAAPGLSGDTGRFLSG FGKFCFGSRKGALLTKGFSVSS GWPAAKFPPAGRVGTVSSRP RRPGKRVL*GEK/GEWAASLPT PLPLAGPSLPSVFQPVPVAPAPOTV RAVSPVTPQGPSSPPLREHSTQ PRPGCREIYQHPRIMGTGRMRTP WPWRLSARPAAAAA

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SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	had	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence	1	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	ŀ			sequence		
3708	34076	A	3748	1279	2791	OAAGGAAGAERDEGAGVA/GA
3700	34070	l^	3740	12/7	2,,,,	HGPSRSTARRGGRGAGPRPPPP
						PRSLGTGSAGRGAAEGTGRAR
				1		RPAGAAAGRALRAGRAGRLGA
į.					ļ	CGGVAAVGARGLRAAAAGAR RRGAPATGAPPP/PSAAASPTAP\
						PGPRHPGRVSGAAARAPPGTAP
		1				RIGERRPGGGAPATEPPDSRTPA
		1				AARASSA/PGAVSGPAAAPGPP
		l				GRRENAEGR*PQDAG*RGLWE
			1			GALPVPGSSPQTSSSSTGRTSGG
	j .	ı				SRAPSHMVPGTGSPPG\RGGEA
		l				GAR*AAAPAGVKPSSLWKK*L
	1			l		ALFRPCFQEPTPG/SVGCRGPLE
		l				CFTHSSPVGV/NGHRHCDNCCR/
1		l				PLKPPSPKAAWAVPRAAVPEA
1		l			1	HA*K*RAEDQRGLRVLGPNVTL
1	1	ł	1			SNPPTRGFR*LGTGVPGFQDPC
		1				VDS/GL*VEEGLCPEASRGNGE
		ĺ	ŀ			RNKGTWGIPPQPPLRPSSRWLQ
		i				E*PTPLPGSP*DATSPPAGGGRH
						RSRLPKPALVGNAGTSSLPAPE
						PCFPHLYFTTFLLSLDSSLKFRD
						LAGILIPE
3709	34077	В	3749	71	285	1
3710	34078	Α	3750	417	1208	GPQRVPTLWWEDAEARSQRDG
		l				VGGRAEAPGARIPRDLGAAGG
			l			LRGHPRLVRGHCRRRLRCSMA
						RTLVLRVTPVPGGAPLALRQPP
						VPGGSRQEWPAFSRVGTGLPLT
						PTAGPSRARGARRPCPPALPGH
						CLLDRTYTGLQTLGAETLLAVV
						NSAAMNVGVQVVDVELHRHS
						LGEDCIYPOSSESDISDAPPSLPL
						TIPAPVKASSPIKOSHEPVPDTS
						VEKGS\PGSCPFHL*GPLSHLGS
1						SPGFLLWRPPGLLSSVALVASC
					L	O. G. EL TIG. GEESS VAL VASC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide tocation of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3711	34079	A	3751	10	932	LQLCSMWLLRSWVQAEGAVSI
					İ	SDSPFSLHQCWAVLHKAWCVF
					ľ	LQLPGGFTFTLNPLSDNLLGKR
1			ł			VDSAPSWGPLGSAFRGVHMPC
			l	ł		VGAAWEGKGPNLLRPSGKLGP
				İ		SGSRPTPIGQQQLPEVPRAKGPL
						GPAAVICQ/HMPAPSTGGKRGS
				l	i	FSGRYLSASLELGGLPMAPTGP
				l	· ·	SALSAPPSVSRGAR*STREKPGV
						YASAT*AAEIREGQALGG\PRPS
						RNG/SGGPLGPDFGPNGPKLRRS
						KAGCPWWHLSSVDAGE*LWK
1						QHSTAVFSMPGTQPPWRGLITM
			1			PISPRGTEPTAHPGPRSPGLAYS
2010	0.1000	Ļ			(50	LTA
3712	34080	A	3752	3	650	GTVLDDPHLTGYCWHPPCPPNS
1				1		VCNGSLSPVLREEAESSEAPVQ
1			1			SPQRSWTPSAKSPPLPASPPCSQ
						LKAGGDQEGLQRGALPVGMD
						RGGPGGCGGHCQCSRPRILSPV
		l				VPVPQVCPSSEAPGPPRQVPHTP
						RPQEPSRTRGRLEA\SAPSWQ*P
		ĺ				APPAGSLPAWP/PG/RPAPTGSR
						AR*AGLEASETTWSTNGPTTVH
		l				P*TL*AGSLGAPQTSAAASEHSP CPNLPLPL*KPWCATNLSCRI
3713	34081	В	3753	1	1812	CPNLPLPL KPWCATNLSCRI
3714	34082	A	3754	1	209	MAQDYGAMGDLVLLGLGLGL
						ALAVIVLAVVLSRHOAP/C*PPA
						FAHAAVAADSKVCSDIGQRTC
						RDATPT
3715	34083	Α	3755	2	462	PPLPGCLGDTGAPWPGPGCTGP
	ļ					PPRTRSPPRLPG*APASRLQNPH
		l				PRGRPWPAGHSRCH*SQPWLA
ì						GPTGS*HLPDASGFCPGALTGS
						CLPSLGGAGGGW\QSAPPDVGS
						KWNTPRRSGAPAPPGGRLLPGP
						ACRAPPRSDLPLS*AGRVGRPG
3716	34084	Α	3756	129	616	NRIFLNCNMVHKCKCKTPMVV
	ľ					AGASLVETGQDESIKDE*LNGIP
						GPVATPSRLPPQRTWN\PGPHP
						MP*RRPQSLPQPSQAPPGPFLS*
						GSEGEGTQPKP/P/GLPGLGPPR
						QPGRCGFAVD/PPRCGVSPGPG
						VPGPAGPAAGAAPG*PKLRQRP
						GPSIGDCGDAP
3717	34085	Α	3757	59	292	YCNVSFGPILSARKPASPRSS*T
						SATWLQNHPLMYLTPGTGTLW
						RFLTTRENVPYGPVP*WNRTIC
						GVANWPYWPSV

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3718	34086	A	3758	177	448	GTGGWVAMLQQYFA/TAWIPH NDGTNNFYTANLANGIAAIGY KSQPALWVTGGLLVIIITFIVRGI VYPLTKSQY\TSM\AKMLVL*P GAEGL
3719	34087	Α	3759	1097	1206	
3720	34088	А	3760	2		QGSRAKLSTPLGISCTRSTAGP SRFARCSLGGCSHPSRHSPHLPP PPPVQFRAGPGRGQGSPSRGSPS GAFPAGPGGAAAAAVGDDQQ QQEQHGAHEGEENNEGNSVPC G/PGKTGGSSVSPGLPEPWPPAP LWTQPSWSAPCHP*KPPIPPTR QVLGRTGCFLLPAP
3721	34089	А	3761	181	581	ADELNVPLT*APAIPLSKEMKL HVPTKPARKRLKWLHSQQPTC PSTGEPVSNCGYPPVPQPTTQQ YQGLDAGATTRVPRSLLRSEGS QTQKSPSCGSHSQDNSGG/SQSS PVTPQHLLSPRAPQAAPSPDRA PV

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WOO	71/0/300/					PC1/US01/08031
	SEQ ID NO:			Nucleotide		Amino acid sequence (X=Unknown,
	of peptide	hod	in USSN 09/540,217	location of first	codon for last amino acid	
	sequence		09/540,217	eodon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
. 1				ordinence.	ł	
3722	34090	A	3762	18	2104	RWQGDKRDSA*RGNLRARKPS
						KRGK/DR*RRVSPTRSGKRRGA
. 1						EEKNRQEKKKGREKERREKRS
.				l	1	ERQRDRRRRKEQRKEEQRRRA
.		l			1	RTNERKPRQTQANGATSS*KAS
		l			1	AQQAGMWGGSP*TDATAIRRG
. 1						GAPCSSRRTCLNQGTIATPSGR\
						RRHGDAG*PGLASEHDASGHG
.						CLRTGAG*PSDSTESVCRRPLA
. 1		ĺ				MHVPTHESHGPVFTRLVSHTFH
.				l		CG\SKLPAVGRPVACRPTYSPSL
.				i	1	CHNPQRPAQLLAHSSALQCAPL
. 1				l		SWDPQRCAPPSPRPHRRGPPSP
. 1				l		HPHRRAPPSPHPHRRA/HTTART
.				1		DPTTSAPPP/RQTQRRATREPAT
. 1		l		l		KHTRNAHPRRSACNRGTHTHP
						RRRRTTERTTHHARPRNRGQAT
		1				PNTRQPTAGRHEETDGATRR
						QHGQTRGEGG/RRRGRAAKTR
. 1		1]		QRERQEPPHDNTRRTRRRPKRR
						DRTGAPAGTRNRTSGHKKRQP
.				i		GTRASTGTAPASQQQQTPTVLS
				l		RCISRFGVFYGPDFSGG\NSFCS
		1				LPLMSDSTLSTYGGQRRG/RSR
				1		ARKTQDTGVLSPLRRERSCPPA
				1		HGRFPGLFLSTHRQVGPAALRP
						PELSCE*LPQDGDFCVWLPSLR
				1		SRLRGTRVVAPASSP/CGDWQV
						TAVAP*PQTQSPSLSQSRDVEK
						RHRGQHPSVGSV*LMKAA*RG
						PSGAKRPKTAPRPQCRARVLPK
						RSGPTSPGRGSCGSQSRTRGF*D
3723	34091	Α	3763	1	446	MWESLELPRDLLNGFDQNADN
						DMDNEIQAEVVSDGDEELVGN
.						WSKGKQLKSSENLQLDDATEK
						KNLFSEEKFKLAEETYLSNEEP
. 1						NINSQDNGKNVSKACQRTLEQ
. 1						AFPS/SGS/GGLGGKNGFVG*AQ
· 1				ļ		SPSAVCSLGTWYP\CPSCCSHG
3724	34092	Α	3764	186	529	GTCWKLEQSTLPLLHWAGLAC
						PLAPGTCTSGPLL/TAPQR*MQL
						CGSPGWHWKRSVVVAPGRQLP
						GSGECMFQLPLPCRQPSLCAIPP
1						ILQANLPLNGRQNCCAQISCKE
			1		1	m Capti
						DQSFH
3725	34093	В	3765	73	1374	DQSFH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
3727	34095	A	3767	603	1208	FTTCSKHQTRPGHRPEQQHPAE KSVSGIFCYAEEMESSQLPDPGS
		ļ.		1		GQPPRGG/ALGPPYEPLSNRIPD
						APG/EAGPASTPGH*SLDQGIPG
						*PGLAPRGHRLWKSPETPAPSP
		ŀ				APRGVSGGLPGSRSAQVGSGDP
		1				SPHHL*QPAAAGRKDSSSF*AT WRPP/GPPGPAAAAGRKDSSSF*
1		1				/GHMASPRPPGPAAAGRKDSSSF*
	İ	i i				FMVLP
3728	34096	A	3768	872	1015	VIRSRMLIPKTMGKVSPGHVRG
3720	34090	<u>۱</u> ^	3700	872	1013	LHSRPSQHRPRGLGGKNGFTAA
		1	1			PAMAEGSNI/GALAVASEGASP
		1				KPWQLPCGVEPS/IRRCMETPG*
1						PGRSLLQEQVPHGEP/PARAAQ
	1	1				KGNVGLEPPSTVPTGVPPSGAV
İ	l					RRRPPSSRPQNGRSTDSLHHAP
						GKATS/SSMPAPESSYEGGGTL
						QSHRGRAAQDHGNPPLASA*P
		1		ŀ		GDLVKLQLLTPQSDNSCTHIGD
		1				NGTYRSQLKAAFAEKLNMGKL
1					l	TFFITGVNHKWGLPLSLTWLPA
						NSWESLLSFPPPSPPQQLNDKPG
1						RRSNITHSSKEDKKTEESLELPR
	l '					DLLNGFDQNADNDMDNEIQAE
	l .					VVSDGDEELFGNWSKGDSCYV
						LAKRLVAFCPFPRDLWDFGLER
	1			1		DDLGYLVEEISKQQCIQEVTRV
						LLKAFSFIRETDHKSSENLQPDN AIENKIAFSKKKFKPVAEICISN
	1					KEPNVNPQDNGESVSRACQRSS
İ			i			QQALPAQAQRPRRKKWFHSCS
3729	34097	A	3769	234	636	GPVSGHHRVNCLPCTILPLRR*R
15/2/	34077	1	15,05	224	050	AKGHLCRLLCPAGEATGARWR
			1			HSPQPLALLQRAPEPAHHHPAA
		ì	l			PPGRLHHAGLRCSPVRPAEEGR
						GPRPQQRARTASLQLLRRR/SLL
						QPQPPD*\RDKMAEPQRRSRQP
ŀ	1	1				AHL
3730	34098	A	3770	1597	1878	DTPRFHSRSKRGITLQEYASSRN
						*RTSSAVPVF*RMSVRGMEVPC
						SNER*TQSISGDQVRPAEEGPGP
ŀ						RPQQRARTASLQLPRRRYFLQP
						QPPD
3731	34099	Α	3771	97	471	GVEELRNVNVFFPHFKYSMDT
			1			YVFKDSSQKDLLNFTGTLPVM
			1			YQA*ICHCWSSSSSSPQVSRGTS
I		1	1			HVFSI\TSDEARQVDLLAYIAK\T
1						LKVFQIQIQRAGQIMRIKQSIKL
3732	34100	В	3772	1	1449	LWLEVENSVLPAH
3132	134100	ъ	12/12	<u> </u>	1777	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \-pussible nucleotide insertion)
				sequence		
3733	34101	Α	3773	I	927	MQRWFNICKSISVIHHINRVKT
						YMIISIDAEKAFDKIQHLFMIKT
						LSKIGIQGTYLHVIKVIYDKPTA
l						NIILNGKKVE\AFPLRTGTRQGY
						PLSQLFFNIALEVLARAIRQ/EEI
						KGIQISKEKVKLSLFAGDMIFYL
						ENPKDSSKKLLELIKELSKVSRY
						KINVHKPVALLYTNSDLVENQI
			1			KNSTPFTVAAKIIKYLEIYLINY
						MKDLYKENYKTLLKKIIDNTN
						KWKHILCLWIGRINLV\KMTILQ
						KAINKLNTIPIKILP*FFTELEKPI
						LKCIQNEKRAHIAKARL/SQKN
						KSGGIRLPDFKLYYKP
3734	34102	Α	3774	1	639	MGRNQSKKAENSKNQNAFSPP
						KENDSSTAREQNWMENEFDML
1						TELDFRRSVITNFSKLKEHVLTH
1						HKAAENLEKRLDKWLTRINSV
1						EKTLNYLMELKTTLFMVDNG/C
						R*LENSHDL*AYFLHLLGNTGL
						*CCVRGQIGDGKEKREQRDSRS
					•	MG/EILRAQLEPFAFHQRSVQC
						GDIRDLWMGYFLLNLMKKLTF
		_				Q*FP*QDT*QLKELKKIAST
3735	34 103	Α	3775	3 .	1079	APGPRGAGAQKACGASAGGDP
ŀ						ECAAY*GGAQCECGPTVGPGE
						VPRAV*VWVHGGPWAGGYPV
ļ						Q*CDAGGREGSFAGAAAAPGG
1						AAGEPAGPCPGAAAAEPAGAG
						AQQPPAGREVCAGDSGPGAAP
					İ	EAGGAGGGAGGTAVPGGDPR
						AAAGPASGPQGPGTAAAAAGG
						RARGTAGAAPRPQGQHAGTGA
						GPPGAAGPARAAAGPAGQRGG
ŀ						TGGGPAGRA*TPDARWASAAG
}			*			PGGGAAEASERARQGSDAAGR
			1	i		VVSGAG*AAG*TRGATGPAGA
			1	l		AGAGAGTAGDAEPAAARVQPA
1				l		AGPERLPADHAV*AIDTAAKCP
				l		GRGEPAAAG*SSGPEPGEQGAP
2726	24104	<u>_</u>	2226	45	140	GAQPGESGPPAPRTAGVPGPA
3736	34104	В	3776	45	149	

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3737	34105	Α	3777	13	442	EGKDERND\GKDEGKDEKKNE
						RNDGKDERNDEGKDEGKDERK
						DERNDEGKDEGNDEGKDD*KD
1					ĺ	EGKDEGKDEGKDDGKDERKDE
				ŀ		GKDEGKDERKDEGKDEGNDEG
					1	KDERKDERKDEGKDEGK
						DERKDEGKDEGKDEGKD\EGK
				l	İ	DEGKDEGKDEGKDERKDEGKD
1				l		EGKDEGKDEGKDEGKDE
		1		l		RKDEGKDEGKDEGKDER
				l	i	KDEGKDEGNDEGKDERKDERK
						DEGKDEGKDEGKDERKDEGKD
						EGKDEGKDAGKG
3738	34106	A	3778	459	660	VRGHEWAQKKYHKFSLWSVD
3750	15	1		1		ST*N*OPSPHASGCHWLEEPAA
		1		l		FCHASPAASGIFAAAASDRPLLP
				İ		sv
3739	34107	A	3779	2	440	RPLSLINIHANFLSKILANSIKOC
		ľ.				LNRIIHHDGVRFIFEM*E*FNIHR
				İ		SINVTYYINRMKNKNMII\DAEK
	ļ					AFDNIQHPFIIKILIKLGIEGT*LN
						TIKALLMAAAACL\NSCCKDAR
						SSRGGMAEGCRLSASSELWAP
				İ		MSMGGGLR
3740	34108	A	3780	1	1145	RHPGWPTPAACPTTLRWLKAP
						VWTPGP/QKMEKEPAARGTPGT
						GKERLKAGASGFAGGMGPRSV
1						PARKKAQTAPPLQPP/RAAPGPE
1						RGAALGRPVAOOVPGARLAGG
						AAGLGFPAVPRVLPPFPCALSG
1					1	DRSARERPPGALLRPLPC*GPPT
		l				PVVGGKNDQLKERADSGPDPV
					1	AADAVPGEAALQARVP/GALGP
						AKLSPEGAIVAPA*VRGPGRLH
					ŀ	OPGLRPGPRORSDPRFPGSREPA
				ĺ		/GERGRGARRGHRRGRPGGPCD
						PRRPGTQGEASERGEAAEGEAA
						EGGET*ER/GGRGKRRGHGPPG
						SPGKPYPSAGSHAKGATGRGH
				l		GTPGTPSPGRSRPGCPRGVPTRS
				l		SGLGVARSSAQARGGTEPAPRR
1				1		SPGAPSGRPATLAK
3741	34109	A	3781	218	376	TRNKILYROANAERFCHHOACP
1,	[,	Γ.		I	I	KG/RS*RKH*TWKGTTGTSHCK
				l	1	NMPNCKDHQG
3742	34110	A	3782	2	187	FTFWHDFAAAGTGCSFPCLVLP
15772	1	Γ`		Ī ⁻	l	SWW*ONLSAFACL*RILFLLHL*
				I		SLVWLDMKCWVENSFL
					l	OL - WEDINICON FERSIE

SEQ ID NO:	SEQ ID NO: of peptide	Met	SEQ ID NO: in USSN	Nucleotide location of first	Nucleotide location of last codon for last amino acid	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3743	34111	A	3783	I	220	IALMVSTIWHVFAVAGTGCFFP CLVLPSGALVRQA*W*QNLSAF ACL*RILFLLHL*SLVWLDMKF WVENSFL
3744	34112	A	3784	713	997	KFFSLRMLNIGPHSLL/CLQSFC Q\RSAVSLMGFPLW\EPDLSLW LPLTFFPSFQLW*1*QLGFL*LLF LRSIFVAFSVFPEFECWPALLD WGSSPG
3745	34113	В	3785	I	1698	
3746	34114	Α	3786	948	1121	
3747	34115	A	3787	1211	2437	LTKRWPGTNTSPESG*SRRAAC AGLLIPFTSRSSSPTWTRPLLS/ ACASSHDPGHHNSP*VLVPPDG GTQGFLVLHQADDLHRFLIKLI DIVRQRRENGVKILLGNRVMY HEHSPQVRGGQQLEQLPLITVH GGGLQLLHHVLSEGHSAVQNW GWTLPFIIAKLLMNLH
3748	34116	Α	3788	1	1908	
3749	34117	A	3789		1788	MTGVSRGSGLPISMAENRRPLY SAGSKPYPILQSPLQILNTTH YELKSLLTPTSSFAHVISSAEDL VQRRNVIGDVYSQGPASPFEIN NGLGSPLKYTAWRKQEMGPW QWLWQQDFHLFLGAFLQRYAE PLPVGTISPGWGSCVVDSSQES LPNDKHLRAAKEVPLQLQWGR SFQLFLGASPQRNTRILLTGMFS WVWLNIHPGTLLGEKLGSWGS KGRTTAGALAERLLVSSESSIFG PREQLEPTAGEPLTEVFRCG*IF QGFCLVKSWGPGAARAEPLQE PRRGCWELLEAAJPGNPEQLP RNAELPLTEVFRCG*IF QGFCLVKSWGPGAARAEPLQE RNAELPLTEVFRCG*IF CGGCSYAAGT PQKAFCPVRSSRARDPCKPFSD CLLGTTDEQKDSSNLCELKCFCL TALKRAVFLPARSWRSENGGT THTTAGSLRSQCDQREEWVSA MEDEMNEMKREGKFREKKIKR KEÇTILQEIWDVYKRPNLCLIGV PESDGENGTKLENTLDDIIGENS PRLARQANGOEIGNTFORNS RATPRHIIRFTKVEMKEKML RAARKGWVTHREKGHIRLTAG LSAETLQARTENGSHILKEK NFQPRISYPAKLSFISGEIKLYFE NFQNSLYPAKLSFISGEIKLYFE NFQNSLYPAKLSFISGEIKLYFE NFQNSLYPAKLSFISGEIKLYFE
	1			I	1	ALNMERNKRYQPLQKHAKM
3750	34118	В	3790	116	885	

SEO ID	leen in No.	Mas	SEQ ID NO:	Nunteatide	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
1	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
1				sequence		
						<u> </u>
3751	34119	A	3791	593	883	
3752	34120	Α	3792	47	716	EAPACL*KALSPLAPTTISSVDC
						GFRASTGITLLPRTGAAHGAAG
	1					*DRGGRAGVLTMTASRACCAG
				l		P*SS*RYLRQ*TPNSLEGPTGRS
	l					LRSRASPGF/TLRDPVTQPSSPV
						AAVS/ALGVEPGLAPAL*SQRV*
	•					ALPR*TRRKSKATAPTATKPNA
	İ					GHNTTKKARPGQGPTPEIPALG
	l					SPREVDPEVAHPGAFLSQPERR
						RCVLGSSFPPGYQQRRVDPLPV
3753	34121	A	3793	2	829	GTRAGWRRRRSGRDGPEVTPQ
1						PPGAARDGAG*TGPSPPRCAGP
1						A/TAAKPSGHPPPGDFIALGSKG
1	İ					QANESKTASTLLTPAPSGLPSER
						KRDAAAALSSASALTGLTKRPI
1		ŀ	1			LSSTPPLSALGRLAEAAVAEKR
		l	İ			AISPSIKEPSVVPIEVLPTVLLDEI
						EAA\SWRATMTGSRACCAGP*S
		ŀ				S*R\$PAP\$LTAP\$T*A\$CTWPR\$
						SPTSSPLRASLRLCVASCGGTPP
		İ				STSRPRGTAWCLCWPVTSSWPP
		-				TRRTRTGPRSLSRCTSRTPWGS
		_				GSGWTALT
3754	34122	A	3794 3795	114	254	
3755	34123	В		860	2052 1090	
3756 3757	34124	A	3796 3797	2252	2557	LNPLSMGRRWPGEETVTDPGW
3/3/	34123	Ι^	3/9/	2232	2557	KRLCHPLHWVAETVPVQAVGA
		ĺ				PWSLQMGGWNWGGRCPQHLA
		l				PSKGVM*RLPGQFGRTPSWKE
						VPEVWGMFRRPACGPRLS
3758	34126	Α	3798	444	854	VSHLEAQK*PSWTC*HQCQWA
3/38	34120	^	3/70	444	0.54	LPMFPHHSEADGLIE*WNGLLK
						SQLQCPPGGNIL*G*GKVLQES
						VYAQNRHLIYGTVSPISRTHRPL
		ŀ			1	CSOSTODSCLLVANPSOICLVHI
		l				PFP*VQHSLGL*ISWDWTGEVG
3759	34127	A	3799	1169	1881	PFL LEHPATVIFCFSWETFDPOGFCF
3/39	3412/	^	3/99	1109	1001	SLPKVSGTCLISLLLHAFPFVVT
34.0	l		l	I		SAPCPQEFPHSPHLCFHVP\HHS
1			1	1		EADGLIE*WNGLLKSOLOCPPG
1	l		l	l		GNIL*G*GKVLQESVYAQNRHL
1			l	I		IYGTVSPISRTH\GHOVTHGOPV
1		1	1			
1	l	1	l	l		KTT/LL*SPSMGSWGIALVLPPL\
1		1		ĺ		DLLLSG*SLTLPLAFLLRTHPLL
1		1		I		TTVQRRAELPFTSWICFLSLFER
1		1		l		GKGPGQPLVTWTECQALTLLPS
2760	24126	D	2000	65	1224	PGSHTQGTWRIPH
3760	34128	В	3800	65	1324	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last eodon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3761	34129	С	3801	I	1263	
3762	34130	A	3802	1	2845	MAPRSLRMEDAIESLAVVSSEY
ľ		l				VGAGVNWMFLPPSSKSTCKILT
						PHVMVLGEQGLAPPTVFLKALP
						IPLYHTVPPGGLQPRAPLVTGSL
						DGGNVPFILSPVLQPEGPGPTQ
		1				VGKPAAPTLTVNIVGTLPVLSP
ŀ		l				GLGPTLGSPGKVRNAGKYLCP
ŀ						HCGRDCLKPSVLEKHIRSHTGE
		1				RPFPCATCGIAFKTQSNLYKHR
		1				RTQTHLNNSRLSSESEGAGGGL
		1		1		LEEGDKAGEPPRPEGRGESRCQ
200	21121	١.	2002		279	GMHEGASERPLSP
3763 3764	34131	A	3803	2	517	KGLAFEVSLADLONDEVAFRK
3/64	34132	I ^A	3804	ľ	317	FKLITEDVQGKNCLTNFYGMG
		l				LTCDKICSMVEK WSTMTEAHV
1		1				DVKTTDGYFFHLFCVGFTKKH
1						NNQILKTSYAQHQQS/RQIQKK
		1				MMEIMT*EVOTNDLKEVVNKL
		1				IPDNIGKDTEKV/CPIYPLHDVFI
						RKVKMLENPGFER\MELRGGGS
3765	34133	A	3805	18	602	PAPWRLACNKRLTKGGKKGAK
0.00		1				KKG\VNPFSKKEWY\D\VKAPA
					İ	MFNIRNIGKTLVTRTOGTKIAS
		1				DGLKGRVFEVSLADLONDEVA
		1		ŀ		FRK\FKLIT\EDVQGKNCLTNFH
ŀ		i				GMDLTR\DKMCSMVKK\WQTM
1						IEAHVDVKTT\DGYLLRLFCVG
1		l				FTKKRNNQIRKTSYAQHQQ\VR
		1				QIRKKMMEIM\TREV\QTNDLK
		i				EVVNKL
3766	34134	Α	3806	525	1173	GEPHSQATSGHFASSAGDTQAN
					ŀ	RVWSGPPANTNRPAAEGHDC*
						KEN*ETERTSTPKPHLYVTIIKD
		l		l		QRKGISD*RSNE*NEARREV*R
				1		KKSKKK*TKPPRNMGLCEKTK
				1		STSDWCT*K*RGEWNQVGKHS
				l		SGYYPGERPQPRKAGQHSNSG
		1		l		NTENATKILLKKTNSKTHNCQI
						HQS*NEGKNVKGSQRERSGYP
		L				QREAHQTNR*SLGRNSTSQKRV

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown.
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3767	34135	Α	3807	111	1329	RNRRRERHKEREGGGTGGTDW
						*RRGNRRKRTQRGRDDERRGR
						DDDONHTTNTRRETTKTKRTT
						NRTOOKREOKRNETSKRNETK
						RATEONRRERTGTRSGRSAKRO
						RTEPERERAARRARAKRTASAA
						RDRGLSSTFQLPTRSGNSVHTS
						KKPLSRKYEODPWADS/GSEGV
						WKPVPRRLEAKVMRESQGSSR
						SCCNSRTSARLITETMR*ATLSS
						NKWSFCMPAGRCLTVTSPCCTP
İ						CALVTRKMLVTLGL*SRSRELT
						T*GTFVRGKQK\SVFSAAWGPG
1	İ					HQAQCSEQPSRGRFHRAQPMA
1	ļ					*EPCCKSRHPRATPLHPRPSRPK
]						SPTTPPPTRQNANNKGHNTTHT
1		1				KPRAPPEPQTTQHEHTPQPPPDS
	ĺ					HAQDNNNKNTPQQPPTKNAER
ł						PPRPTAHPPPAHKPLL
3768	34136	A	3808	2	517	
3769	34137	В	3809	1	1008	
3770	34138	Α	3810	139	1407	WRGGLDSALRAAVTLQGCAGC
į.	ŀ					DRPGSA*SNNYSI*I*R*RW*SN
				1		YSEK**GNEGNAVILLFHSNGT
				1		ASKWTVNRASADISKSLQASW
ł						GTEHTWPEGEYS\AGPSQHSSP
		1				AVSDSLPSNSLKKSSAELKKILA
l				1		NGQMNEQDIRYRDTLGHGNGG
				1		TVYKAYHVPSGKILAVKVILLD
		ĺ				ITLELQKQIMSELEILYKCDSSYI
İ		1				IGFYGAFFVENRISICTEFMDGG
		ļ				SLDVYRKMPEHVLGRIAVAVV
						KGLTYLWSLKILHRDVKPSNM
						LVNTRGQVKLCDFGVSTQLVN
	ł	1				SIAKTYVGTNAYMAPERISGEQ
		İ		1		YGIHSDVWSLGISFMELALGRF
	ł					PYPQIQKNQGSLMPLQLLQCIV
						DEDSPVLPVGEFSEPFVHFITQC
	1	İ				MRKQPKERPAPEELMGHPFIVQ
						FNDGNAAVVSMWVCRALEER
377 I	34139	В	3811	1	1134	
3772	34140	A	3812	374	931	WRGGLDSALRAAVTLQGCAGC
						DRPGSA*SNNYSI*I*R*RW*SN
						YSEK**GNEGNAVILLFHSNGT
1	1	1	1	i		ASKWTVNRASADISKSLQASW
	1	1	1			GTEHTWPEGEYS\AGPSQHSSP
			1	l		AVSDSLPSNSLKKSSAELKKILA
						NGQMNEQDIRYRDTLGHGNGG
				1		TVYKAYLCPEWENIICKGHTTR
						YYTGTSEANYV
3773	34141	Α	3813	3	444	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				sequence		
3774	34142	Α	3814	75	807	GIAGFVNIHLDSLSFLTGVPGVK
						AERF\E*RMTAKHCALSLVGEPI
			l	l		MYPEINRFLKLLHQCKISSFLVT
						NAQFPAEIRNLEPVTQLYVRVD
ĺ				l	ļ	ASTKDSLKKIDRPLFKDFWQRF
				l	l	LDSVKALAVKYLQRIGSRTPM
			l			DTKIYSYCPAVHPAEPTDMKS
						WPSLFEVPTSLEYCPFYLQLVES
			İ		l	ADAEGTQKYRRLTAYYIPVYTE
			l	i		PPLITKEPSCLWKQAEFGDLGK
1				1	l	HVWLVEQFSSTRVQEHGVGW
3775	34143	Α	3815	35	2088	KVMNKRSQTQNGTRYMTPPPR
				l		SSHTKQHLL\PTPPPRSSHTKQH
					l .	PLHDPITTKLTHRT/CTRYTTPSP
						RSSDTEQHPL\PAPSPRSSDTEQ
				i		HPL\PAPSSRSSDTEQHPLHDPT
	İ					TTKLTYRTAPATRPHHHEAHTQ
	1					NSTRYTTPSPRSSDTEQHPLHGP
1						ITTKLTHRTAPATRPHHHEAHT
						QNSTRYTAPPPRSSDTEQHPLH
						GPTTTKLRHTTAPATRPHHHEA
						HTQNSTRYTAPSPRSSDTEQHP
			1		ł	LHGPITTKLTHRTAPAT/PAPSP
				1		RSSHTEQHPL\PAPPPRSSDTEQ
				•		HPLHGPTTTKLTHRTAPATRPH
						HHEAHTQNSTRYTAPPPRSSDT
						EQHPL\PAPPPRSSHTEQHPL\PA
						PSPRSSHTEQHPL\PAPSPRSSHT
						EQHPLHGPITTKL/STQNSTRYT
						APSPRSSDTEQHPL\PTPSPRSSH
						TEQHPL\PTPSPRSSHTEQHPLH
1					1	GPITMKLTHRTAPATRPHHHEA
i				1		HTQNSTRYTAPSPRSSHTEQHP
l				1		L\PAPSPRSSHTEQHPL\PAPSPRS
						SHTEQHPLHGPITTKLTHRTAP
			1	I	l	AP/PTPSPRSSDTEQHPLHGPITT
	1		1	1		KLRHRTAPATRPHHHEVQEQA
	1			1		KPIK*PPRPSPETTRAQPREPAV
1			1	l	l	TLLPSGALGQACPCDATAGPHG
				l		TTLWPAVPPRWQQHLTRELLH
	1			1		PVPRACP*QGQGQPFTAGPGRG
2006	24444	<u>. </u>	2016		104	SHPYDPTGASPKGQSSIL
3776	34144	Α	3816	83	184	RLTLPDRLGSPPDTH*AQHITRA
L	L		L	l	L	VLPQGFTDSPH

SEQ ID NO:	SEQ ID NO: of peptide sequence	hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3777	34145	A	3817	1	811	MAEEDSGNLQPEGEGEAGTSS HGGAGERYKGKYLJTFKQPDL TKQTRFIRGPKTPAPVTDWEGS LPLVFNHCRDASLIHPHFKGVR PRRDACLGPSPLAASPAFLGKG QHALKRLKPHTRLLQHGLLKP NSPYNSPILPVLKPDKYKLVQ DCLINIHULHPHAVPNPYTL LSSIPASTTHYSVLDLKHAFFTIP LHPSSQPLFAFTWTDPDTHQAQ QIT*AVQPQSFTDSPHYLNQAQI
3778	34146	A	3818	2	324	SSSSVTYLGIILHENTRALPADH HFEARRQAGPPKPSPQPPFR*LP TAGT/RGGGGEKAAGGFRWGR FAG/MGQGPDPPGAHGQNPASP SLDFPWGPICASQGVTDQSPSTF OGPLGEA*KPTAGAKPGAGAG
3779	34147	В	3819	206	1391	(
3780	34148	A	3820	229	792	LGSSAGNSAPDPWRPTSSGVFS FHNTSHSHWILRLRTGERSEV CVQGTWPTBLWALPPPFFFFS PAPAAFASCQSLPPHSPQSPRPG AGISRPRSQEAPDSSQ'PAPTRP SVPSPMANGGGDDRQPPTRPD TPPRPNAASQSAGHNYASLPAP RGRVGVGIGFPGSPACAGGGIW HFHTLSPPAF

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SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3781	34149	A	3821		1676	KDNERRLNTCRSTRSHKRAHTR RSIRAHRGSAAAPPAAQAPGW RWASSCPRVOSAAGRGGRGGA ASGR*APRWGCPP*CGSRFGKC SPSPAPLASTPPRFGTEPPCCL*R GTCLGSACSGSGGRG*RR*GTG TORRCPLPSARPRTRRQISCOG KFS*CPSASSTNVCSPTGRGL*K PVPWAPGGRRRRPS*GRSSGDL SSGTWWP*S**ELGIPEYSHST/G GLVGVAMPPHRRAVTGNVHIA GQARKKDSPIGGRSPAWL*SPL FCAPGGRGGASHLLLSFP*ESYABFYC GWRFARPPESABKSIGGRSR GWRRARPPESABKSIGGRSR GWRRARPPSAGTRGNRTSSS WRAPWRFGLGTGEPPGAPPG FASSPRRTPISSLSPAGSGGGS LGRRQRAADRARTKPGGD*VG SWAGRRPPGGAEGF*QGRPPPA YAVLLLSGWPGGEGGGSLQPS VQLLVQGGPVGLTG*VSPRLLT REALKQNGATEAGGEHWPSCP PSH*/PGAGEHPGAADTLQVAS PA*GHGTAGRGGRAPAAHPAH RGORAHSTRO
3782	34150	С	3822	78	371	
3783	34151	c	3823	349	591	
3784	34152	A	3824	822	2114	AGRSVRIQAMTCLIPPAHLGYP GSPQAPESSCPQO*GRMHSQPT PAGRRMOGDEPSFSNNIGVAG PGAMSRYTCPGCKNSNQRTEEP KKMR*TF*SLSSFPWGSGSPHP VPSFLWVPPSQLPNT*KLRAGL GTSGLAPGGTOKLEFMRASLV VEGVAE*RQGLGTAGSGHQPE RTGHRLWPAASG*SLACSAPSR KGSCFSRSLSRSTETSLPAPGSL SAVGH*GVESAWPAAGRAGNH FCPEVADNLYEMKPPEPQVKP GSWAGRPPGGAEGP*GQIGGP GLTLSFFFQGGPGGPGGPGGPGGPGGPGGPGGPGGPGGPGGPGGPGGP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO; in USSN 09/540,217	location of first codon for peptide sequence	codon fur last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3785	34153	A	3825	3	452	PRHSPGCRCPVAEGQSSGRALP PRLILLAVLLLLLCGVT/CWLCP VLLPPEAGTGPATSATSTAALR
		1				CGSHPYGQ*QPCTQ\P\GPPTAP CSTHWACGCPAFGSWNWTPW/
						PPPAYSLYTPEPPTSYDEAVKM
2704	24754	Ļ	2024	1,	110	AKPREEGPALSQKPSPLLGAS
3786 3787	34154	A A	3826 3827	292	118	SWQELESRAQAPNVGORDGPR
3788	34156		3828	2	462	SWELESSANJANVORLUGH RGLSYHVAAEVNELLVEGQHR LEGDKHFTGHSG*QGARGVKA GRDP*PRGLVKAVGRGAMES RSSSPKGRGNRMPSGVCTEL*A AGNGSGFVEAGLAFTPAISTPT LPRRRAAVLVADVAGPVPASG GSRTG/AQPAVTP\QAEAGGPPA G*APLATGCSGPRAGTGPRGR SCRPRSPAPPAAAAGAAAA AAAAAVRGRSAAPCP GPVSIGEPEIGPPOPVSIGEPE*G
2780	24157		2820		274	PPGPVSIGEPEEGPPGPVGIGEPE EGPPGPVSIGEP*EGPPGPVSITE PE*GPPGPVSIGEPEEGPPGPVGI GEPEEGPPGPVGIGEPEEGPPGP VSIGEPEEGPTGPVSITEPEEGPP GPVGNEMSSR
3789	34157	A	3829	3	374	YRAL VFSSSTQ*VSKNFLYSGSS SMLPVLASFFLSFFLAIFWNGA NSATAGYSRPQVGGEELEVVV CWQRAQLLLQLLLGEARRQAA DDHLRGARGRSHRGGAWTRSS KGTAYRAGRPGPRPTK
3790	34158	Α	3830	66	619	VRSLESEMNVVEFONGFWNMF PVKRPKISCSGRVCSIPEDSQKE AEKKRCQDWKHRR*SRI*EVPR NLRVEEEKTSANPETLLGEME AKTRELLARETTPLLEVIKNRKL EKORIREEKREERRRELEKKR LREEEKRRISVEDR WL YTIKINR RKSQRKK*GLRSHSGSDKEHRD VERSQE
3791	34159		3831	253		QVSTCYHSQEKEKKRISSTSKSL NKEKRRNEQ\KDQ*ALLSSPPSP PAESQGWHWSSLPPIISRFLKTS YILDLDIKK
3792	34160		3832	156	443	
3793	34161		3833	426	513	
3794	34162	В	3834	47	1311	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence		Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3795	34163	A	3835	1503	1652	NCGNNQ*LTNQKKSRSRWIHS QILPDVQGGAGTIPSETIPINRKR GNPP
3796	34164	Α	3836	I	1986	
3797	34165	Α	3837	I	1116	
3798	34166	A	3838		546	ERSSPAAEOSWMENDFDELRE EGFRRSNFSELKEEVRTHGKEV KNLEKRLDKWLTRITHTQKSLK DLMELKTTARELHDECTSLTNQ FDQLEERLISNFSKVSGYKINIQ KNIKHSYTPITDKQRAKS*VNS HSQLLQRE/YKYLGIQ'AYNGCE GPLQGKLQTTAQGNKRIQTNG RTFHAHG
3799	34167	A	3839	1	987	
3800	34168	В	3840	i	1593	-
3801	34169	c	3841	1	1479	
3802	34170	Α	3842	129	368	
3803	34171	В	3843	1	1884	
3804	34172	В	3844	1	471	
3805	34173	В	3845	1	675	
3806	34174	Α	3846	1	410	
3807	34175	A	3847	250	880	GEVTKPOFAGFHIGSLASLTIRE GKMESGKVISCLQACKEGLDIN SLESLGQGIKYHFNPSQSILVME GDDIGNINRALOK VFYINSKQPF TAGVRRLEVSSKVQCFGEDVCI SIPEVDAYVMVLQALEPRITLEG TDHFWRPAAQFESARGVTLEG IKIVSTFAKTEAPGVA*KPQVQN SEFSL*AFENPVSCQISNSGHVP NFOFRV
3808	34176	A	3848	890	4889	
3809	34177	A	3849		799	MYAQPPNCKREKASGDVSLYW WKLAKGCLQMEVSEGARNSAS TPTGNTVSQELNRPLPIQPPYPR RFSWYCRSSLQA*VAESATKTS AFRAPNSFCRLQPRFCCRASPAS PATSCTCPGSLAWARPAPSH PATSCTCPGSLAWARPAPSH PATSCTCPGSLAWARPAPSH PATSCTCPGSLAWARPAPSH PATSCTCPGSLAWARPAPSH PATSCTCPGSLAWARPAPSH PATSCTCPGSLAWARPAPSH PATSCTCPGSLAWARPAPSH PATSCTCPGSPCTSPRPPRGRDA PER*AHCPPVPDA*FGALAPQA TGGGQPPGAQPHHARAGPGVG RTPLQ*GCLCARPGEPQLRVTPH GPQAGG/ITTGRLPPMGKPGVSG GVCPHSDFPOPMFTVEMTGPRS GVCPHSDFPOPMFTVEMTGPRS GVCPHSDFPGTGWLAPDAESLV SFEFSSPT*VL*QQWK*RSGVQR PT
3810	34178	Α	3850	212 .	361	

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nuclcotide
1	sequence	l	09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
3811	34179	Α	3851	3	909	GGRQRGKDTGHMAKQEQERE
15011	5 1175	ľ.			, , ,	VGGATHL*TTRFRSCSK\SALIP
1						VIPITKSTGSRFRNSVEGLNOEIE
						IIIKETGEKEEOLIPODIPDGHRA
						PPPLVQRSSSTRSIDTQTPGGAD
						RGSNNSSRSQSVSPTSFLTISNE
						GSEESPCSADDLLVDPRDKENG
						NNSPLPKYATSPKPNNSYMFKR
						EPPEGCERVKVFEECSPKQLHEI
						PAFYCPDKNKVNFIPKSGSAFC
		1				LVSILKPLLPTPDLTLKGSGHSL
1						TVTTGMTTTLLQPIAVASLSTN
1						T\SKTESLEEQVQSCHQLLYSHH
1						ONOLRKLKD
3812	34180	Ā	3852	189	454	LWKRFNSWTSLRHPYOPYOAE
13012	34100	^	3632	109	434	QIAPQTCGSQSDGGLPSSSGPAP
		ĺ			1	LHHAGLGYGTEGSPGARRRVE
1				ì		GODP*VLEOAAGPTPPRYLVRP
3813	34181	Α	3853	17	561	IPGSWROKMPVPPAA\PAHAOG
13013	34101	^	3655	11'	301	RPGALOSPGSSTPAOPGSRWEV
i				1		GGPAAPWGSLRHP*OPYOAEOI
						APOTCGLOSDGGLPSSSGPAPL
						HHGGLGYGTGGSPGA/LEEGGR
						PRSLGPGAGSRAHAAEVSFPSG
						PPSRGLTGSGFCACSEERAGFPR
						ELMVIKNTVTPTREATTLILTKA
						PAILP
3814	34182	Α	3854	1	540	FFOPIFWGKDPOSGTPPHP/RPG
15014	34102	ľ.	3054	ľ	370	PAPSGPEPSISMVTRRWLRAPN
						CSDRRGEGPRTEADRHGSCCRF
						RSRAGTAVHSCRRRHPRAAGLP
	l		l	1		SSLCAEAGPRET**LEGGCREG
			l			AEPRP*RPGSGAHAHTDPERAH
			l			RSGARTO/HPERAHRSGARTOIR
						SAHTDPERAHRSGAR\HRSGAR
		l	l			
						RTLPL

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \-possible nucleotide insertion)
				sequence		
3815	34183	A	3855	1326	2409	GRPPGVPPATAPRAAPGAGDGE
			1			AGTPAPGDHPEPVCRIOPG*WG
						T*GWGASQHWGGH\PALALAG
		1				RRPSRGLAGASGRSSEEPGVAT
		1				QRLWESMERSDEENLKEECSST
				1		ESTOQEVLALEEERAQVLGHVE
1						QLKVRVKELEQQLQESAREAE
				1		MERALLQGEREAERALLQKEQ
	ŀ	1		l		KAVDOLQEKLVALETGIOKER
						DKDLQRQCCGMMGDRAKASP
		1			1	SWTSTVILKFPLIKNCLNPKDIS
		1			1	LMAKELWSLRTMDALNRNQIG
		l				PGCQTQTMVQKGPLDLIETGK
						GLKVQTDKPHLVSLGSGRLSTA
						ITLLPLEEDCLPSLVDDLVPRLG
l						LKISLETRRRGOLMLCTPKFEN
						QWPTTDKMPETSTGSH
3816	34184	Α	3856	240	639	DHGRSQ*EPNRPWMPDPDHGA
3010	34104	ľ^	3030	240	039	ERTLGPDRDRORAE\MOTDKPH
1		l				LVSLGSGRLSTAITLLPLEEGRT
						VIGSAARDISLQGPGLAPEHCYI ENLRGTLTLYPCGNACTIDGLP
						VRQPTRLTQGLSMSLPSQLIQET
3817	34185	-	3857	1	1758	MALLPTVLCLWAQAQVGVQR
3817	34183	Α	3837	1	1/38	
			İ			HNHIFWNEKEHGHGKSGSCHN
	ļ.		i			GASCSAEDGACHCTPGWTGLF
						CTQRKPHLLASQPLRIPCCGLL
1	l					ATVGIVQTSREGGMQAAPGLV
						VPDSCPTRTEELCRGSSRPDWIQ
1						GIDKPKVLQGCPAAFFGKDCGR VCQCQNGASCDHISGKCTCRTG
1						
						FTGQHCEQRCAPGTFGYGCQQ
1						LCECMNNSTCDHVTGTCYCSP
1						GFKGIRCDQGIMLLLFLIV/CAA
						GPICLASAAAEREGPRPGSPCLL
					ł	HTCHE/R*PAPTTPSQDLTDHYL
1		1				RFSMPIMVLT/CLQGAFPGSPGR
1			1			\PG*TWAPLCGMNVNRPGT/HE
		l			1	LGCDSDHWGPHCSNRCQCQNG
1						ALCNPITGACVCAAGFRGWRC
						EELCAPGTHGKGCQLPCQCRH
1						GASCDPRAGECLCAPGYTGVY
	l	1				CHPVTGACTCQPGWSGHHCNE
1	l		1	1		SCPVGYYGDGCQLPCTCQNGA
						DCHSITGGCTCAPGFMGEVCA
	1		1		i	VSCAAGTYGPNCSSICSCNNGG
	1	1	1			TCSPIDGSCTCKEGNVPSLPSPS
	1	1	[LTYEHIPQVVLPAEGSQDGTFG
		1				LNCSEHCDCSHADGCDPVTGH
L		1	l _			CCCLAGWTDIQEGFLEKEGPKR
3818	34186	Α	3858	2	2414	

SEQ ID		Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X-Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3819	34187	Ā	3859	I	852	DEEEVVAREEEEEEEEEMVPE
3617	34167	^	3037	l'	032	ESMASAGPEDFEQDGEEAALA
				l		RGAPAVDSLGMEEEVDIETEPV
						AHEKRPSMLDEPPLPVGVEEPA
						DSREPPEEPGLSQEGAMLLSPEF
						PAKGLAHPNGSOKVIFRVPLRV
						IHGPKAVELQVFPGLHKOPTNO
			-			PK/TEPCDPHSWFKSCYHLLFIP
		İ	ļ			VGISRPP/HNPTITATIFASTASV
	ŀ		Ì	l	1	LW/PVLDTCMSSNSGYFKAVLE
		ĺ				SYSSKVLSVTOYGNPRATGSAG
]				LRGRPGS\PGSSGSRGPAWP*PO
		1				AAPRCPPSSGRPGPTSOSPS
3820	34188	A	3860	3	1997	AOGSVVPGLFWAFLOLEVNCL
3620	34100	^	3000	ľ	1997	LESPIIQGKFHFRLERISVVEPQE
		l				RKRLSFRKSEI*P*K*SLVKKL*E
		1				RLKTRKOMOLANRLRRYGYSV
		l			•	VES*FPNLKVSSSVSTTPTTTYIP
						MTHKAIFSSYFLWDGRSAFLTI
		ŀ			i	YKMMSSHPOEEEEEEEEGGE
					'	GEERKRRKKEEERGKRRKRRR
						RMK*RRRRTRKRRKRKMK*R
		ŀ				RRRRRRNMRKKRKEGKNMKK
						KM/REEIKRONALYEIEMRKKL
				l		EKKREEMHESRRRFLAPLFSSP
						TANCSTSLVPRLRLASLPAALPS
						NR VVR VTTPPAG VRGA WRHSH
						FSRSRSIMDTSSEMLVRFGRRC
						GRAKESTGRDWNSLKSSEEDR
						KMWESLELPRDLLNAFDONAD
					-	SDMDNKMQAEMVSDGDEELS
						GNWSKGDSCYVLAKRLASFYL
				İ		CPRDLWNFEKDDLGYLAEEISK
			ŀ	l		OOSIOEAORSRRKKWFYGPGPG
				İ		SLCCVQPIDLVPCVPAAPAMAE
				[RGOCRAHAVASEGGSPKPWOL
						PHGVEPVGAOKSRIEVWEPPPR
						FOKMYGNAWMSROKFAAEAG
						PHGEPLLGOCRRELWGRSSHVE
				ĺ		SLMGHYLVELLSIGAMGIKVOR
				I		PRCFFDIAINNQPGEKGTGKSTQ
						KPLHYKSCLFHRVVKDFMVQG
				l		GDFSEGNGRGGESIYGGFFEGP AMGPNATNNFTKLAG
				L		AWGENATINE IKLAG

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SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence		
3821	34189	Α	3861	86	1120	LVLSKGKEHLLGIKEHEEEEER
302.	31.07	ľ.,	5001			RKKYE*KDAEEIKRONALYEIE
		1		ľ		MRIKLEKKREEMHESRRRFLEH
		l l				MQDKHIIKAVEQQQ\RQRKKM
1		l				KR*ENSSKQKKRLIQMGKEKEA
		1				ETHRLMEKRRERIHNFLSELLK
	1	1				EKLDNEDMIIARDIAEAEAEWE
1	1	1				KREREKDEKNQAELKTIAEYRA
1		1				IVMKNKEEEERQRKIEAKEQLL
	ļ	l		ł		AVMKADQIFWEHEKEKKCKA
						DKEHQEVQDAHIQQMAKNKFN
						AKQAKQAELDYCRLTEALVAE
l	1	l				KEKEFQDYAREVIELESETPNK
		1				YIYPLVKAVQEGPGGGRGPVFV
		1				DRGGLRPSYQANDVTGVQLPF
1	1					YNSQGPKYNFQKSKRRLGFTW
3822	34190	A	3862	591	2805	WVHQPAGS*GEKPT*ISAPPWP
15022	151176		5505			EAPTSELWVLTPPEAVQEAAAR
	1					VGQEVPAAP/RGPLPSSATGAK
		1				SLGQGSPTPSTRSMSLQSCAGP
!	ŀ	1		İ		OHP*TLRRGPLWGTSRWKMVL
		l				T*ASRTSSTPGLT/QGPRVTVLL
	l	l		1		GKAGMGKTTLAHRLCOKWAE
		1		1		GHLNCFQALFLFEFRQLNLITRF
		i		l		LTPSELLFDLYLSPESDHDTVFQ
	l					YLEKNADQVLLIFDGLDEALQP
						MGPDGPGPVLTLFSHLCNGTLL
						PGCRVMATSRPGKLPACLPAEA
1	1					AMVHMLGFDGPRVEEYVNHFF
		1				SAQPSREGALVELQTNGRLRSL
		l				CAVPALCQVACLCLHHLLPDH
1		l				APGQSVALLPNM/YSALYADG
						ARPQPPWALAHLV/LYWTWGR
	i	1				WP*GAWRQGRLSSMQKILLHP*
		1				*LLGPLTAC*LPSASAQALGTS/
		1				ETGYAFTHLSLQEFLAALHLMA
		ı				SPKVNKDTLTQYVTLHSRWVQ
		l				RTKARLGLSDHLPTFLAGLASC
1	1	1			[TCRPFLSHLAQGNEDCVGAKQ
1	1	1			1	AAVVQVLKKLATRKLTGPKVV
				1	l	ELCHCVDETQEPELASLTAQSL
	1.	ı			1	PYQLPFHNFPLTCTDLATLTNIL
	1	l				EHREAPIHLDFDGCPLEPHCPEA
	1	l				LVGCGQIENLSFKSRKCGDAFA
	1			1		EALSRSLPTMGRLQMLGLAGS
	1	1				KITARGISHLVKALPLCPQLKEV
	1	1		1		SFRDNQLSDQVVLNIVEVLPHL
	1	1		1		PRLRKLEQGRSGAPGVGDSTPD
3823	34191	Α	3863	ï	2784	

SEQ ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3824	34192	Α	3864	727	1715	YLSKGLKEVREGSLQIPGEHPG
	l			l	1	RKKLMQMLSEKTL*SQHHY*K
	I					GFLQRQIHQKMIAHLVEQRNK
				ł		DCMFLQIMPAATS*/TEIQATIR
				1		DYYKHLYANELENPEEMDKFL
		1		ł		DTYTLQRLNQEEVESLNRPITG
	i			l		SEVEAIINSLPTKKSPGPDGLTA
	İ					EFYQRYKEEL/PKPCRDTTKK\E
	1			l		NFRPISLMNIDAKILNKILANRI
				l		QQHIKKLIHHDQVGFIPGMQG
İ						WFNICKSINVIQHINRTKDKNH
İ						VIFSIDAEKAFDKIQQPFMLKTL
l						NKL\GIKYPGIQLTRDVKDLFKE
						NYKPLLSKIKEDTKKWKTILCS
						WVGRINIVKMAILPKAPLPLPP
3825	34193	В	3865	1	1908	
3826	34194	В	3866	609	1658	
3827	34195	В.	3867	61	234	
3828	34196	A	3868	1	978	LFTDDLCQPVEATSGQAMVQS
ļ						RGATTHGGGRGGSCKLLGDRG
	İ					QGSTSQVGRWGSSCHPPTGG\P
			ł	ŀ		ARSPCWPTARKPLRGVLQGASL
	l			i	1	GSTASMLGAASGTPRPPPSWLV
		l				SVPSPRAPCWGVPGAG\EQGGP
l						ETQPPGAREYPQPAGREGRPQI
						LRFPKSSSSQCLVEFCSLASSCF
						ALEAMKTRRSPSS/SGSSGSDG/
						SQRTTRSGPAQRPRVSGSSEQG\
l				l		DGMRGGSSGGMKGRRVPKREP
						RTEAASSSTA*RQPPPPPSPLPH
		l		l		ARRHFRFRPCCGPARDAAPSRA
						QTEAPPPLRTQSALSWPLCSRT
				L		DGKLSRGQSRDGSRAPTPGVL

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SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	endan for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
3829	34197	Α	3869	1	1919	TPVSDEEEGSLHHTTWRNLRIG
						VRIACPAGENAQSSESPVRACQ
		l				PGTŔTQYGLNQAWSPGVRRDL
l		1				IQGSAERPARYPAPGEMGVGAF
		l	l			IPLGHDKRRAASQHLHVSGREG
		1				PEALGSRGSALRKQVPAWLPHS
		l				LRTCPVDRNPQAPCARTGLMV
		İ	1			ETPHHEQWVRGEHYRYKFSRP
		l				GGRHAAEGKWWVRKRIGAYFP
		l	İ			PLSLEELRPYFRDPHTLMLGQR
		1				VTERELDGEPRGPVTVEGRSAT
		1				TSGYPTKVTKIGGPLDPAGGLE
						GPLHGALGSDPLEVSDCPGPHL
1						SRKVWENGSFGASDQQHTR/YT
	İ	l				TDGSSWPTVAEKKAPSSKQYH
						SSMET*R*TGHSNHPRNRPTCG
						QVPPNENNTRNRPTHTARYLPT
	İ	l				/ENNPRNHSTHATRYLLTTTTTE
				i		IIPHAARYRPTRTTRYLPTRTTR
	Ì		-			YLPTKMTREIVPHAATYLPMRT
1						TREIIPHTATY/ASNENNQYLPM
1			ļ			RTTSQVPSNEDNPGCLPTRTTR
						HLPTRTTRYLPTRMTQEIVPHV
l						AWYLPTKALRPFNGKRTAFSA
l						NAAKRSEAPTLR*ALRT*CPVN
						PPDTEGTGPAMPSLECPEQGNP
						QRRWAGRRRSSGAQDAGQGTR
		1				FTPSLWRAWGWSRLRPRLSAP
		l				GCWLTRKCRTEPPVVPQALMM
						AAVTDMQTLIH
3830	34198	Α	3870	295	457	
3831	34199	Α	3871	296	1057	GNEVKMPARETTPHRVPTGAQ
		l				PSEAGEKGHHPPDRRMVDPLTL
i		l		1		ALCTWKSCRHSMPDCKAAGRE
		l				AVPCKVTGAERPRPRAPTSA*P
ŀ		1				SGKLEGLSLWCTQSCSCMLHR
		1				AGVISVFFTMEDVAPTRGLLH*
				1		RAAIGIISPITISVTKTSNNCRWC
	1		1	1	İ	RVGGCAN*LRGALEAGG/WLQ
1		1	1			NQKGRDAFNKRLRGGMDKPG
1		1		1		AGGTCGSGRRNRPLRDRS/VPE
1	1		1			VKGGTGTG*KTGSGGLKRKYV
				L		GDGTTASFESLRVLIKWPL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3832	34200	٨	3872	3	913	GGADSGERLGPHALGLGAGSG GGRGRYGPSSRSPSGRAADPGG KPFFPVAPRGARARRGGRVVP AF*RPAGAA*AAQIHIVVVSEP AAAARGGGPGGQOSRAWRG KRLFGGAGGLAGPPGRYPVL GPPGSGPAAGRPGQGAGQ EPPPAGDAAAAPSSGSASCR/G PGAA/GPRALCPGPAPPARRGPR AGLGRPAADRGAPAAAPVRAE PHGLGGAAGARPPHRLRGGAG HSGALVLITLWITGGGGGDGD RASPGSPGPLAT/GAGLVGNKAFSL
3833	34201	A	3873	2	484	TSQCPCPQL TPWRRKSTE*PTLGVRRPVPRN AMPHHCSFFTGRTVPSMATPG YNEGWDKFRMKCHLCVNYIE MQTDPANCDYVIVSGAQRKEE RWDMADNEQVLTTEHEKKQK LETDAMFRLEHGEADRSTLKK ALAHT)DHIQEAQSAWKDDFAL
3834	34202	Α	3874	3	531	NSMLRRERYPSKP GRKRSKRNBKGERGEPYSLSLR NHQGSWEPEHMS*KPEGGIVLA FKGDDGFSVWESNAIATYVSNE ELWGSAPEAAAQAVQWVNFA DDSQYGGVPTLGKMHHDKQA TODAGGEVOPOFOAVLGEMK LCENMAHFDAKIFAESQPKKDT PRKEKGSREEKQKPQAERKEEK KVATPAP

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SEO ID	lego in No.	Mot	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3835	34203	A	3875	2	1326	TMAAGTLYTYPENWRAFKALI
3633	34203	^	30/3	12	1320	
						AAQYSGAQVRVLSAPPHFHFG
1				ł		QTNRTPEFLRKFPAGKVPAFEG
	ŀ			1		DDGFCVFESNAIAYYVSNEELR
	ľ		İ	1		GSTPEAAAQ\VVQWVSFADSDI
				1		VPPASTWVFPTLGIMHH\NKQA
ŀ	1	1		1		TENAKEEVRRILGLLDAYLKTR
						TFLVGERVTLADITVVCTLLWL
		1				YKQVLEPSFRQAFPNTT\RWFL
	1					TCINQPQFRA\VLGEVKLCEKM
	1	l		1		AQFDAKKFAETQPKKGTPRKE
				1	,	KGSREEKQKPQAERKEEKK\AA
	1			1		APAPEEEMDECEQALAA\EPKA
	İ			1		KDPFAHLPKSTFVLDEFKRKYS
		1				NEDTLSVALP\YFWEHFDKDG
	ì					WSL\WYSEYRFPEE\LTQPFMSC
		ı		1		NLITGMLORLDKLRKNAFASVI
1		1		İ		LFGTNNSSSISGVWVFRGQELA
	l	l				FPLSPDWQVDYESYTWRKLDP
	1	i		1		GREETQTLVREYFSWEGAFQH
	ł					VGKAFNHGKIFK
3836	34204	c	3876	58	222	r Gigit Milokii K
3837	34205	A	3877	6	153	
3838	34206	A	3878	2	889	CPPWELILDOFRKSLGISPANTG
15050	31200	ľ.	5070	ľ	00,	PLCPAPPSCMYPPSPOMPAKAP/
	l	ļ		1		PDHPPEGRPGTTPEPFPRVTCVT
	l	1				E/PVGKGLSRDSQ*ETRGDLQE*
				l		SLAAPKSAPCFTHSAICPGAPSM
1		l				SRHPERSVFLLFOAPVOEPPAPG
	İ			I		PP*WVLREPDFGTGVFPEPSW*
1				į .		
ı		1				KAADFEPLGLCPGRSLSAQCPS
1		1		1		WWPPTSSDPG*ALLKSGTGTPT
		l		1		VAPRQPAPAAPRFQRPPQPRGL
		1				ASTCPAGPQQKGSDPPGRSAGS
						E/GSVSGKSLKPCLSSPLIPPPQS
		1				STQKKASVAKFVEFSPYTKQKS
						QLSVP
3839	34207	Α	3879	1	391	MAKAVEKPESTLEATKSKESV
		1				MSRVEWIGTAHMWVDDETGD
		1				NASKTQQTLEPAELATKYANFS
1		l			ľ	EGACKPGYASALMTAIFPRF\C
1		l			ł	KPIRLSP*PRHLAHWCKKWAPK
		l				ILGSSAPVALQGAAPVAALMG
1				I		WR
3840	34208	Α	3880	1	346	
3841	34209	Α	3881	249	474	VYLLIVLAVLYTNNRQTESQIM
1				1		SELPFTIASKRIKYLGIQL\TRDV
						KDLFKDNYIPLLKEI*EDTSKW
1		1		1		KSIPCSWI
3842	34210	A	3882	25	302	
3843	34211	Α	3883	1	2235	
<u></u>					<u></u>	

SEQ ID NO:	SEQ ID NO: of peptide sequence		SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3844	34212	A	3884	1	2724	MGGMVESSRHNWSGLDKQSDI QNLNEERILALQLCGWIKKGTD YDWGPFLNSL VQEGEWERAAA ALFINLDIRRAQILINEGASSEK GDLNLNVVAMALSGYTDEKNS LWREMCSTLRILQLNNPYLCVM FAFLTSETGSYDOVLYPEKKVAV RDRVAFACKFI.SDTQLRYTEK LTTEMEKGANLEGILLTGLTKD GVDLMESYVDRTGDVQTASVC MLQGSPLDVLKDERVQYWIEN YRNLLDAWKFWHKRAEFDHR SKLDPSSKPLAQVFVSCNFCGK SISYSCSAVPHOGRGFSQYGVS GSPTESKVTSCPGCRKPLPRCA LCLINMGTPYSCPDRSTROKV NKDIQELNSALHQADLIDIYRTL HPKSTAYTFFSAPHHTFSKIDHI VGSKALLSKCKTFEITNCLSDH SAIKLELRIKTFTPNRSTTWKLN NVLLNDWYNHEMKAEIKMFF ETMENKOTTYQNL WOTTKAVF
3845	34213	В	3885		1971	RGKFIALNAHEKIQTTIREYHK HLYANKLENLEEMIKELDTYT LPRLNQEEVESLNRPITGSEIEAI LNSLPTKKSROPDGFTAELYOR KREELVPBLKLFOSIEKEGILP NSFYEASIILIPKTGRDTTKKEN FRPISLMNIDAKILNKILANQIQ OHIKKLIHNOVGFIPGMOGWF NIRKSINVIQHINRTKDKNHMII SIDAEKAFDKIQQFPMLKTLNK
3846	34214	A	3886	1	11146	METRPSRGPLTPHTARCQSETK LPEGSGSNICCSAIFAILQPPLV IPRQTGSGVDLQQTPTDLELRD LTVRKKTKKWKGIASTSTKRTS TPKRHLSWFFEKINKIDRPLAKL IKKKEKRHOJDI IKNDKGDITTN PTEIQTTIREVYKHLYANKLEN LEEMDKFLDTYTLTRLNQEEVE SLNIPITVSEIEAIIKSLPTKKSPG PDGFTAEFYQIASIILNGQKLEE FPLKTGTRQGCPLSPLLFNTVLE LITRITIRGESTKGIJQLGKEEV KLSLFADDMIVYLENPIVSALN LIKLISNFSKISGYKINVQKSHA LIKLISNFSKISGYKINVQKSHA
						RIKYLGIQLTRDLKDLFKENYK PLLNEIKEDTNKWKNILCS

SEO ID	SEO ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleatide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
1				sequence	İ	
3847	34215	A	3887	66	1392	OVLLSFGTPLVLTTKREKNOID
3647	34213	^	3007	00	1372	AIKNDKGDITTDPTEIQITSIEYY
		i				KHLYANKLENLEEMDKLLDTY
					l	TLPRLNOEGVESLNRPITGSEIE
		1				AIINSLRPISLMNIHAKILNKILG
				l		N*IQQHIKKLIHHDQVGFIPGMQ
	į.					GWFNIRKSINVIEHINRTKDKN
						HMIILIDAEKAFDKIQQPFMLKT
						LNKLGIDGTYLKIIRAIYGKPTV
		Į.				NIILNROKLEAFPLKTGTROGCP
						LSPLLFNIVLEVLAKAIROEKEI
			1			KGIQLGKEEVKLSLFADDMIVY
		1				LENPIISAQNLLKLTGNFSKVSG
		ì			1	YKINVQKSQAFLYTNNRQTESQ
						IMSELPFTIASKRIKYLGIQLTRD
			1		1	VKDLVKENYKPLLKEIKEDTNK
						WKNIPCSWVGRINILKMAILPK
						VIYRFNAIPIKLPMTFFTELEKTT
İ						LKFIWNQKRACIAKSILSQKNK
						AGGITLPDFK
3848	34216	В	3888	I	2868	
3849	34217	Α	3889	I	1218	
3850	34218	Α	3890	I	1893	MKEIETQKTLQKINESRSWFFE
						KINKVDRPLARLIKKKREKNQI
			ļ			DAIKNDKRDVSTDPAVIQTTIRE
						YYKHLYANKLENLEEMDKFLD
				į.		TYTLPRLNKEEVESLNRPITGSE
			i			IEAIINSLPIKKSPGPDGFTADFY
				l		QRYKQELVPFLLKLFQSIEKEGI
1						LPGSVYEASIILIPKPGRDTTKK
			1			ENFRPISLTNIDAKILNKILANRI
						QQHIKKLIPHDQVGFIPRMQS\W
ľ			1			LEVLARAIRQEKEIKG/IQLGKE
						EVKLSLFADDMIIYLENPIISAQ
1						NLLKLISNFSKVSGYKINVQKS
						QAFLYINNRQKESQIMSELPFTI ASKRIKYLGIQLTRHVKEHFKE
		1	i			NYKPLVNKIKEDTNKWKNMPC
						SWVGRINIVKMTILPKIERIGKT
			İ			KGTETQRGKSCKPTHPVSVISL
ļ		1	Ì			AESIARDFCLQLNRARSCDQSS
ŀ	1	1				YNEVLEADNRAFSLCKGMPFD
			i			RLSPISQTPGPSWYQSSPYQPMF
			1		1	LAAPIDIGSRPASMDPIHSRTWH
			1	1	1	YVTVVILARSRKHQELILSESKQ
					1	FEEAPPELRSRAPGGFSKPAAG
				I	1	QIKVGLRENLTASMQISPADAN
					1	LILODSFLAIFLFOALIVTIYKEN
					1	EKEEGOERREEALRSTGKNNV
	1	1	1	1	1	WKNTDIDRPESISDSESAGCDY
				L		WICH DIDICI COIODOCOAGCOT

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X≈Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
	ŀ			scquence		
3851	34219	Α	3891	2	1562	WGEIRAEKLKIPKTGAPLFLORI
15051	3 1217			Γ		AAPROORNKTGORMSLTS*OK
						*ASEGR**OT/LSKLKEHVLTHC
	l					KEVKNLEKRALAKLIKKKREK
1						NOIDAIKNDKRDITTDPTEIQTTI
						REYYKHLYANKLETLEEMDKF
			1			LDTYTLPRLNQEEVESLNRPITG
			l			SEIEEIINSLPTKKSPGPDGFTAE
						FYORYKEEL/PDKOLOQSLRIQ
						NQCAKITSIPIHQ*QTNREPNHE
						*TPIPNYYKENEIPRNPTYKGCE
						GPLQGELQTTAQR\KRGHKQM
			İ			EEHSMLMDRKKQYCENGHTA
				İ		QGSTDFGEVQRLRLWQEDDVA
						EEVSGFFEEDNLKSVAQDPFWE
						SRQVKTIFNCVDTYIAGAKAIA
1						GITQVTCTGNQFAEINQRFLKL
1						KKSWSLYRRFQPWQEECGPSW
1						NPSWTHPSVASSRKDAAAQRE
				i		AQEGDLQGQEGAEASHAGGPA
				1		ADHYSGTAHAGRGRALDRGVC
						VRGHAPPPITELSRPAGCGPHR
						QGEEAREGDANKKNGFHIQRC
						SCCLSCKQEHPVLPLVFGLD
3852	34220	Α	3892	2428	6109	YPESTMNSNKFTRKKSNNPIKK
i						CQQASQLKALPTQSCSPSSNSY
						ETFLVSPLHPFQFYISFPHYTEM
1				İ		VPPLTPEDYNSRGDFGGDTETN
i				ŀ		HIISKFHRSLEQVQNAASRRSQ
1						DGRIGTAPVYSSQRERRRRRVIS
1						AFPSEERSSSPAMEQSWMENDF
						EELREEGFRRSNYSELREDIQTK
	ľ			ŀ		GKEVENFEQNLEECITRITNTEK
İ				ŀ		CLKELMELKTKARELREECRSL
		1		ŀ		RSRCDQLEERISVMEDEMNEM
l						KREGKFREKR
3853	34221	С	3893	13	391	
3854	34222	A	3894	117	704	WLSAWPRACPDCRVRFPHTSPP
1				l		CLPCGPEAEPGPGPALRELVQP
				[LPGQLQPPFGMPLPLVPAGSFLI
				İ		CTVWERPRPGLAVGSPPCFPSL
1	1			1		H/PTVPVGCPPPSPCL\RPPA*PT
1	l					THLHIWPSLLFGPLPALPPPLAA
1	I					SASAGLRKPWLDGLHPSVEPSG
1	İ			1		LGAAPSPAPPACA WTRPPHLHP
1						SSFSSCVPQISSLFLCF
		_				· · · · · · · · · · · · · · · · · · ·

SEQ ID	SEQ ID NO:	Met	SEQ ID NO:	Nucleotide	Nucleotide location of last	Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop eodon, /=possible nucleotide
	sequence		09/540,217	codon for peptide	of peptide sequence	deletion, \=possible nucleotide insertion)
				sequence		
2055	10.1000	 	lanes.	ļ	1185	la i data sana penangan a sana
3855	34223	Α	3895	11	1185	SAASSVLYVHNEPQVHGAHQK
ŀ			l		1	IHPIHPSLHYCLAHIISQDLHTS
		1	1	!		MNALGLFGVG*EQGLQEKSNL
						SSTHHEPGHGGQDAAGARDGA
		1		l		RGRGGS\TGSAAGERGGRTVPH
				l		WA/GQPAEAGGAG*PRGPQLRF
		1				SPPP/RLPPRAGSSANTRNSVLL*
		1		l		FF*AVCLWADHYPL*TLISSS*M
				l		AGR WRS VPGIPTSPTK/PPPPPPP
		1				PPPPPPPPPPGSFLSEP\VWSTA*
		1	1	l		NSTCPPRRCRSASGGPIWCPCRF
				!		/PAPPPAPPAPPPLEATEESLEEG
				l		\GGRASRSANMFAPTAPAGSSW
		1	İ			HRARWG*PAWKAGAAGTRGA
ŀ						KCGQFVPSASSAP*LAGGWPGA
		l		l		GGQRGARRAQKAWCCRPGTSL
ŀ				l	1	/APGPELFPESALVQAGSAPPPP
i		1		l		PPPPPPPLCLLLLRAESEGAVLM
3856	34224	Α	3896	192	477	
3857	34225	Α	3897	2	1782	RAAARKEHQGSAT/RAERA/PR
		1		ĺ	l	TPKAS\GRG\SPVPTSGTVTART
		1				GTAPRGLSAEDGRRRGRP\IGIP
		i		l		FTDHSSDILSGLNEQRTQGLLC
		1		ŀ		DVVILVEGREFP\THRSVLAACS
		ł	ĺ	l		QYFKKLFTSGAVVDQQNVYEI
ŀ		1		l		DFVSAEALTALMDFAYTATLT
1		1		l		VSTANVGDILSAARLLEIPAVSH
		1		l		VCADLLDRQILAADAGADAGQ
		1		1		LDLVDQIDQRNLLRAKEYLEF/
				l		YYQSNPMNSLPPAAAAAAASF
		1		1	i	PWSAFGASDDDLDATKEAVAA
		1		l		A\VAAVAAGDCNGLDFYGPGP
		1		l		PAE\RPPTGDG\DEGDSNPGLWP
l		1		l		ERDEDAPTGGLFPPPVAPPAAT
		1		l		QNGHYGRGGEEEAASLSEAAP
		1				EPGDSPGFLSGAAEGEDGDGPD
		1		1		VDGLAASTLLQQ/MDVIGGPGG
l		1		l		G\RGGGQRRGVAGRRQGRHGL
1		1	1	I		LPEVLQRRPRRRRLPGLVAEGG
1		1		[EEDPSQGLPEVPHLREGHPGRR
1		1	1	l		QAAATHPHPHGREALRVQHLQ
1		1				GPLHODTSTSTLOKPGSPRPL*V
1		1				TAGR*AGQAEGAHAEAHGREA
1		1				VPVPAVRRRLCPOLRPEEPHAR
		1		1		AHGPAPLPVRQLLQDLRPLRPP
1				ĺ		AQTPQERRLQRRPLAPAVPASP
l						CVLWAGGCPDPQPW
3858	34226	c	3898	162	356	
2020	- 1220	1~	10000	1		L

SEQ ID	SEQ ID NO:		SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3859	34227	Α	3899	3	2289	GELHGVAEQAEGDPREGSPGP
		ŀ			\	AEQASGTELREVPGPHWPLHPP
		ŀ				EAPVCQHYHRPMVQKGN*GSV
		ŀ	l			WGRGESLVQG/AHGQTSQRSV
		ŀ	l	ŀ		OMTGGGAWTGQTSQRSVOMT
		i i				GGGGTPRGSRSSSPRTT\TPGTA
		ĺ	i			EDTEGEPAGAGEQAAGRPVRP
		ŀ				LHGHPGAGQEAAAGVRELPPA
		ŀ				EPAAHLHPQPALLIQQHPISHAR
						SOHPRRPCCLPGPGLRAGGTAE
		1				GLPCAFCSQRDERAEGRERDLE
						GGGEAASGPGRQAQAPGQGGH
		1				LGPPLTPAAPLPWWLEGHHRE
		1				ATGRPRGG*GRPPGRGPTGRRK
						ASRAODISSGONLPRGHPA*VA
			ŀ			SPRHEPPAHLOPA ARDHCRGA\
			ŀ		\	PGSQACPADRGPANGTPPPLPA
		į	ļ	1		RSSPPSP\GMSVASPWTASCGPP
		1				GPPP*P\IGPEALPEGGPALPPKP
	1	1	1			PPVPAPSEPPQQPPGPCCSPQRP
		1				PAPGPEGORSRGLGGAHRTAG
		l	ļ			AAOCPGGHAGPSPGGGTAPAP
		1		ł		GPAAAAG*GOGROCOAKGPAH
		1		1		TRGDAALPTSRLRL*GP*E*GD
				l .	1	OGSSG\AAGLSGGRHTOPAGPG
		1				RAORTEAAATODCALDKPLDL
]		i		SEWGRARGODTPKPAGOHGSL
				i		SPAAAHTASPEPPTOSGPLTRSP
		1				OALSNGTKGTRVPEOEEASTPM
		ł				PPDLDGHP\GPARLKC*DQSPTN
		1				WMRQTPQAA\SGPELPGGG\PT
		1				STTGEGPECICTOEHGOGPPRK
3860	34228		3900	3	3169	ASQLVLTLAYQANCVSVSYTD
3800	34228	Α	3900	13	3109	LLGKPGGSYFTFLYVLNIRSRSR
		1				LKKDYDDFRRQPDHDTFNREL
						WTTDEGEGDLGKDSPKGEISKS
		l				
				İ	l	IDSTEPLDILEKDHFDSDDMKLS
		1		I	1	EIDFPMARSKLLKKELPSKDLP
			1	l	1	KTLLKTLKRQSKQTDYVDDST
		1		I		KELSPRKKAKLSTNETTVENLE
		1	1	l		SDVQIDCFSESKHTEPSFPESFA
		1		l		SLDSVPVSTLQKGTKPIQALLA
		1	l	i		KNIGNKVTLTNQLPPSTGRNAL
	l					AVEKPVLSPPEAS

SEQ ID			SEQ ID NO:			Amino acid sequence (X=Unknown,
NO:	of peptide	hod	in USSN	location of first	codon for last amino acid	*=Stop codon, /=possible nucleotide
	sequence		09/540,217	codon for peptide sequence	of peptide sequence	deletion, \=possible nucleotide insertion)
3861	34229	A	3901	33	1227	HHLRGTGQRAGQQLPPGMKM
			1			GRAGPPGPWCEHTT/PPSRGRPT
						SSGGPTLAPALAELSPRPQTPSP
			l			SISSLPMITSLPGGTGPLCLRPLS
İ			İ			WEKPGSATGK\RGSQQEVDVG
						PSPGHTAPSKSHGQGPVGSPSA
						RQGCGPASSALQRRREPGGGPR
			l			GHPAGPHGGCVLPPWPGCPGN
						TMQRL*GFHTRAMNTQSGAGP
		l				RTAPSPRAQGAQGRPSKSCSGA
						SQGPCPAVGPH*APGEDRVRHP
		1				LASISGTTRAHGRPSQQREPRN
						KSTRADSRSPRTVPPHGPPGPSL
						PRGR\PAQPGPGV*RNGISVGAG
			ł			RFPPFTAPCGQQARPGAG\NRG
						AGSGA\PEL*GGLGRDPGSSGCE
						VPGGRAGG/PPRT*HFLARPAPP
						SPPQGLPRPPKVLGLQA*ASAPS
3862	34230	Α	3902	124	1183	DNRAVFSPTGRR\DRGGGGPAG
						TLARV*SAPGAFGV*STRTHVA
		1				GVQMPPVPGTCDVCTRPCSPVS
			ŀ			RPPRASTAVAAAAS/SGPRQPR
		l				HPRHTSPMPPPAALRPPAGPRG
						LAPGG/HTAPPATAAPVELQHP
						LLRLQTGPPLGPPTGPA*EPRAH
						PCIRGLLPAGSGPPPRRQGHPEP
						PRLHTAACSPCQPQRALESSCPP
						RAFPGTAAHWLLGTGDWLL*P
		ĺ				AAQAALASQEWALPGICLCNSL
ĺ						SEPTGRVILASQLAPCIRLGCRK
		l				RSLAKAPKLISGGAGAHTPTPE
						PTCFSVSVLGTSPPAAGGPRGQ
						ESVVSSPVTMGT/VPAWAIPSLG
	1					CRGEASLDHPAGQLPARGQRSR
						RH

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